

Figure 2

|→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←|→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGTCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTCAACAAATGTGCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCTGGAGCTGCAGTGTGAGCCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

FLEX←|
A T A P T A P
0526 GCCACAGCCCCGACAGCCCCG 0546

Figure 3

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACCTATCTCTCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→Flex
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCTGCTGGTCCAAGATGCAAGGCTTGTCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAATGTGCTTTTCAGCCCCCCCCAGCTGTCTTCTGCTTCTGCTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAAGCTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGCCTGGAGTGCAGTGTGAGCCGACTCTCAACCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

Flex←→hinge hinge←→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGAGCCCAATCTTGTGACAAAACCTACACATGCCCAACCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCTGCGTCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGC 1050

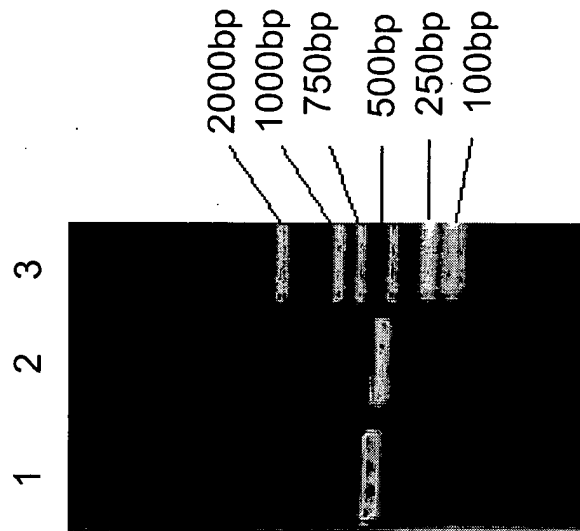
N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCGAGCCGAGAACAACTACAAGACCAAGCCTCCCGTGGTGGTCTCGAGCGGCTCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCGTGATGCATGAGGCTCTGCAC 1200

CH3←|
N H Y T Q K S L S L S P G K
1201 AACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAA 1242

Figure 4

G G G G S G G G S G G G S
GGCGGTGGAGGCTCTGGTGGAGGCGGTT CAGGAGGCGGTGGATCT



Lane 1: mSM5-1 heavy chain variable region
Lane 2: mSM5-1 light chain variable region
Lane 3: DL2000 DNA Marker

FIGURE 5

Figure 6

[illegible]

Figure 7

0001 ATCATCACCAGAACAGCTTACGAGCAGACCGCCAGACAGCTCACAGGGATCAAGCTTGCCGCCACCATGGAATCA 0075
 I→SP
 M E S
 0076 Q T Q V F L S L L L W V S G T C G N I M M T Q S P
 SP←I→V_L
 CAGACTCAGGTCTCTCTCCCTGCTGCTCTGGGTATCTGGTACCTGTGGGAACATTATGATGACACAGTCGCCA 0150
 0151 S S L A V S A G E K V T M S C K S S Q S V L Y S S
 TCATCTCTGGCTGTGTCTGTCAGGAGAAAAAGGTCATATGAGCTGTAAGTCCAGTCAAAGTGTTTATACAGTTCA 0225
 0226 N Q K N Y L A W Y Q Q K P G Q S P K L L I Y W A S
 AATCAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCC 0300
 0301 T R E S G V P D R F T G S G S G T D F T L T I S S
 ACTAGGGAATCTGGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTTACTCTTACCATCAGCAGT 0375
 0376 V Q A E A D L A V Y Y C H Q Y F S S Y T F G G G T K
 GTACAGCTGAAGACTGGCAGTTTATTACTGTGTCATCAATATTTCTCCTCATACAGTTCGGAGGGGGGACCAAG 0450
 V_L ← |
 L E I K R
 0451 CTGGAATAAAGCGG 0465

Figure 8

→SP SP←→VH
M E W S W I F L F L L S G T A G V H S E V
0001 ATCGCCGCCACCATGGAATGGAGTTGGATATTTCTCTTCTCTCTGTCAGGAAGTCAGGTGTCCACTCTGAGGTC 0075
Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
0076 CAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATAC 0150
T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
0151 ACATTCACTAGCTATGTTATGCACTGGGTGAAGCAGAAGCCTGGGCAGGGCCTTGACTGGATTGGATATATTGTT 0225
P Y N D G T K Y N E K F K G K A T L T S D K S S S
0226 CCTTACAATGATGGCACTAAGTACAATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGC 0300
T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
0301 ACAGCCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGCGGTCTATTATTGTGTCTACGGTAGTAGGTAC 0375
VH←→CH
D W Y L D V W G A G T T V T V S S A S T K G P S V
0376 GACTGGTATTTAGATGTCTGGGGCGCAGGGACCAAGGTCAACGTCTCTCAGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTACGGTGTCTTGGAACTCAGGCGCCCTGACCAGCGCGCTGCACACCTTCCCGGCTGCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGCTGGAAGCAGGCTCAGCGCTCCTGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCTCTTCAACCGGAGCCTCTGCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAAECAGGCCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCTGACCTAAGCCCACCCCAAGGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAATCTTGTGA 1125
K T H T C P P C P
1126 CAAACTCACACATGCCACCGTGCCAGGTAAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCGGTGTGACACGTCCACCTCCATCTCTTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAGCCAAAGGTGGGACCGGTGGGTGGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCTGTCAGAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCCGTGAGTGGGAGAGCAATGGGAGCGGAGAACAACTACAAGACCACGCTCCCGTGTCTGAGT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1951 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 2025
S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGGTAATGA 2021

Figure 9

0001 ATCATCACCAGAACAGCTTACGAGCAGACCGCCAGACAGCTCACAGGGATCAAGCTTGCCGCCACCATGGAATCA 0075
M E S
SP
0076 Q T Q V F L S L L L W V S G T C G N I M M T Q S P
SP←|→V_L
0151 CAGACTCAGGTCTTCCTCTCCCTGCTGCTCTGGGTATCTGGTACCTGTGGGAACATTATGATGACACAGTCGCCA 0150
S S L A V S A G E K V T M S C K S S Q S V L Y S S
0151 TCATCTCTGGCTGTGTCTGCAGGAGAAAAGTCACTATGAGCTGTAAGTCCAGTCAAAGTGTTTATACAGTTCA 0225
N Q K N Y L A W Y Q Q K P G Q S P K L L I Y W A S
0226 AATCAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCC 0300
T R E S G V P D R F T G S G S G T D F T L T I S S
0301 ACTAGGGAATCTGGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTACTCTTACCATCAGCAGT 0375
V Q A E D L A V Y Y C H Q Y F S S Y T F G G G T K
0376 GTACAAGCTGAAGACCTGGCAGTTTATTACTGTCTCATCAATATTTCTCCTCATACAGTTCGGAGGGGGACCAAG 0450
V_L←|→C_L
L E I K R T V A A P S V F I F P P S D E Q L K S G
0451 CTGGAATAAAGCGGACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 0525
T A S V V C L L N N F Y P R E A K V Q W K V D N A
0526 ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCC 0600
L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0601 CTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0675
L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0676 CTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG 0750
P V T K S F N R G E C Stop
0751 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAG 0786

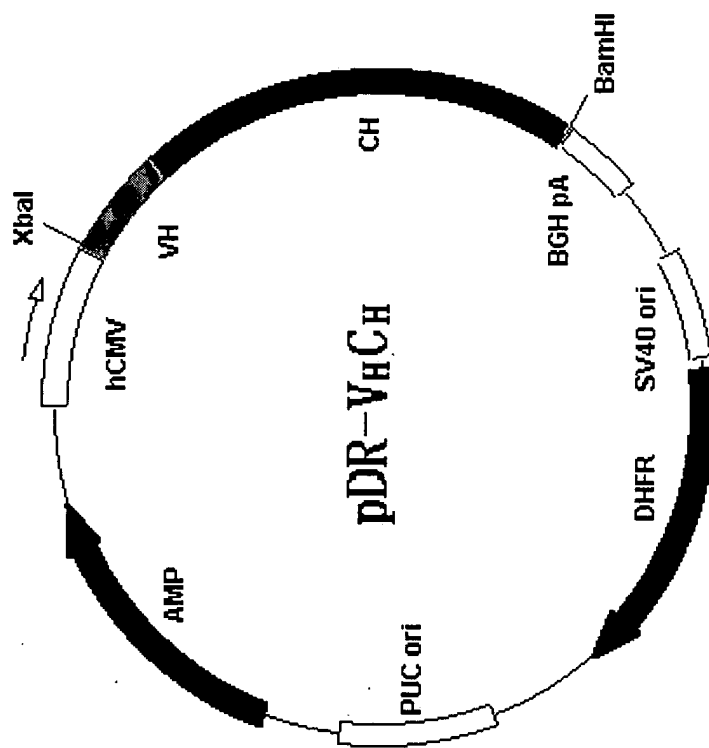


Figure 10

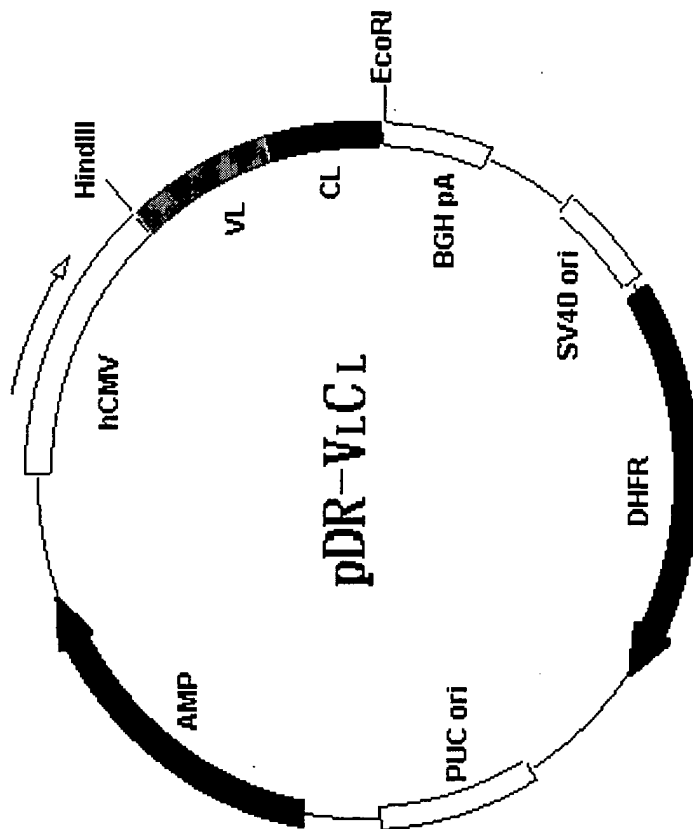


Figure 11

Figure 12

	→SP	M D W V W T L L F L L S V T A G V H S Q V	SP← →VH
0001		AGAGCCGCCACCATTGGATTTGGGTGTTGGACCTTGCTATTCCTTGTGCAGTAAGTGCAGTGTCACCTCCCAGGTG	0075
0076		Q L V Q S G G G V V Q P G R S L R L S C K A S G Y CAGCTGGTGCACTCTGGCGGTGGAGTGGTCCAGCCCCGGCCGAGCCTGAGGCTGTCTCGAAGGCATCTGGGTAC	0150
0151		T F T S Y V M H W V R Q A P G K G L E W I G Y I V ACCTTCACCCAGCTACGTGATGACATGGGTGCGCCAAGCCCCGGAAAGGCCCTCGAATGGATTGGCTACATTGTG	0225
0226		P Y N D G T K Y N E K F K G R F T I S S D K S K S CCTTATAATGACGGTACTAAGTACAATGAAAAGTTCAAGGGCAGATTTACAATATCAAGTGACAAGAGCAAAGTCA	0300
0301		T A F L Q M D S L R P E D T A V Y Y C A R G S R Y ACCGCATTCCTCCAATGGACAGCTTGCGTCCAGAGGACACCGCGGTATCTATTGTGTGCGCGGCAGCCGTTAC	0375
0376	VH←	D W Y L D Y W G Q G T P V T V S S z GACTGGTACTTGGACTACTGGGGCCAAGGCATCCAGTCACCGTCTCTCTCT	0426

Figure 13

```

|→SP
M D F Q V
0001 GAGCATTACCGGCATACCTCATCACCATCCCAGGATATCTCTAGAAAGCTTGCCGCCACCATGGATTTCCTCAAGTG 0075

SP←|→VL
Q I F S F L L I S A S V I M S R G N I M M T Q S P
0076 CAGATTTCCTAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGAAACATCATGACTCAGAGCCCA 0150

S S L S A S V G D R V T I T C K S S Q S V L Y S S
0151 TCCAGCTTGAGCGCATCAGTAGGCGACCGCGTAACGATCACTTGCAAATCCTCTCAGTCAGTATTGTACTCCAGC 0225

N Q K N Y L A W Y Q Q T P G K A P K L L I Y W A S
0226 AACCGAAGAACTACTCTGGCCGGATATCAGCAGACTCCCGGCAAAGCCCCAAAGTTGTCTGATTATTGGGCCTCC 0300

T R E S G V P S R F S G S G S G T D Y T F T I S S
0301 ACGCGCGAGTCTGGCGTGCCATCACGCTTTAGCGGCAGCGGGTCCGGTACAGATTACAGTTTACCATTAGCAGT 0375

L Q P E D I A T Y Y C H Q Y F S S Y T F G Q G T K
0376 CTGCAGCCTGAGGACATAGCCACCTACTACTGTCCAGTACTTTAGTTCCCTACACTTTTGGCCAGGGAACATAAA 0450

VL←|
L Q I T R .
0451 CTGCAGATTACTCGA 0465

```

Figure 14

→SP SP←→VH
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATTCTCTGTTGTCACTAAGTGCAGGTGTCCACTCCAGGTG 0075
Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGCAGTCTGGCGGTGGAGTGGTCCAGCCCGGCCGAGCCTGAGGCTGTCTCTGCAAGGCATCTGGCTAC 0150
T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACCAGCTACGTGATGACATGGGTGCGCAAGCCCCGAAAGGGCCTCGAATGGATTGGCTACATTGTG 0225
P Y N D G T K Y N E K F K G R F T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAAGTTCAAGGGCAGATTACAATATCAAGTGACAAGAGCAAGTCA 0300
T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCTCCAAATGGACAGCTTTCGTCCAGAGGACACCGCGGTATACATTGTGTGCGCGGAGCCGTTC 0375
VH←→CH
D W Y L D Y W G Q G T P V T V S S A S T K G P S V
0376 GACTGGTACTTGGACTACTGGGGCCCAAGGCACTCCAGTCACCGTCTCCTCTGCTAGCACCAAGGGCCCATCGGTG 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCCCTGGCACCCTCTCCAAAGAGCACTCTGGGGGACACGCGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGGAACCTCAGGCGCCTGACCAGCGGCGTGACACCTTCCCGGTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCAAAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCCTGCTGGAAGCAGGCTCAGCGCTCCTGCTGGACGCATCCCGGTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCTCTTACCCGGAGCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCGAGCACAGGCTAGGTGCCCTAACCCAGGCGCTGCACACAAAGGGGAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCGTGACCTAAGCCACCCCAAAGGCCAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGTCCGGACACCTTCTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAATCTTGTA 1125
K T H T C P P C P
1126 CAAACTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACAGCTCCACCTCCATCTCTTCTCCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCACTGGTACGTGACGCGG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAAGTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAGAACAACTACAAGACCACGCCCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGTCTCTTCTCTCTACAGCAAGCTCACCGTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAATGA 2021

Figure 15

0001 GAGCATTACCGCCATACTCATCACCATCCCAGGATATCTCTAGAAAGCTTGCCGCCACCATGGATTTTCAAGTG 0075
M D F Q V
|→SP
SP←|→V_L
Q I F S F L L I S A S V I M S R G N I M M T Q S P
0076 CAGATTTTCAGCTTCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGAAACATCATGATGACTCAGAGCCCA 0150
S S L S A S V G D R V T I T C K S S Q S V L Y S S
0151 TCCAGCTTGAGCGCATCAGTAGGCGACCGCTAACGATCACTTGCAAATCCTCTCAGTCAGTATTGTACTCCAGC 0225
N Q K N Y L A W Y Q Q T P G K A P K L L I Y W A S
0226 AACCAGAAGAACTACCTGGCCGGATATCAGCAGACTCCCGGCAAAGCCCCAAAGTTGCTGATTTATTGGGCCTCC 0300
T R E S G V P S R F S G S G S G T D Y T F T I S S
0301 ACGCGCGAGTCTGGCGTGCCATCACGCTTTAGCGGCAGCGGGTCCGGTACAGATTACACGTTTACCATTAGCAGT 0375
L Q P E D I A T Y Y C H Q Y F S S Y T F G Q G T K
0376 CTGCAGCCTGAGGACATAGCCACCTACTACTGTCAACAGTACTTTAGTTCCTACACTTTTGCCAGGGAACATAA 0450
V_L←|→C_L
L Q I T R T V A A P S V F I F P P S D E Q L K S G
0451 CTGCAGATTACTCGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 0525
T A S V V C L L N N F Y P R E A K V Q W K V D N A
0526 ACTGCCTCTGTTGTGTGCTGTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC 0600
L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0601 CTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0675
L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0676 CTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG 0750
P V T K S F N R G E C Stop
0751 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGITAG 0786

Figure 16A

→SP SP←→VH
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATTCTGTGTGTCAGTAACTGCAGGTGTCCACTCCCAGGTG 0075
Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGCACTCTGGCGGTGGAGTGGTCCAGCCCCGGCCGACGCTGAGGCTGTCTGCAAGGCATCTGGCTAC 0150
T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACCAGCTACGTGATGACATGGGTGCGCCAAGCCCCCGAAAGGCCCTCGAATGGATTGGCTACATTGTG 0225
P Y N D G T K Y N E K F K G R F T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAAGTTCAAGGGCAGATTTACAATATCAAGTGACAAGAGCAAGTCA 0300
T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCTCCAAATGGACAGCTTGGTCCAGAGGACACCGCGTATATACTATTGTGTGCGCGGACCGCTTAC 0375
D W Y L D Y W G Q G T P V T V S S A S T K G P S V
0376 GACTGGTACTTGGACTACTGGGGCCAAGGCACTCCAGTCACCGTCTCCTCTGCTAGCACCAAGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGTGTCTTGGAACTCAGGCGCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCCAGCAACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGCTGGAAGCAGGCTCAGCGCTCTGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCCTCTTCACCCGAGCCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGGCCATATCCGGGAGGACCTGCCCCCTGACCTAAGCCCCAACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTCTGTCAGAGCCCAATCTTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCCCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACACGTCCACCTCCATCTCTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGATCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCAGAACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGCAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGACACGAGTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCAAAGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CGACCTCTGCCCTGAGAGTGACGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACCACTACAAGACCACGCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGAGGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K T Q D
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGTAACCCAGG 2025

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
2026 ACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

D Y P V T V A S N L Q D E E L C G G L W R L V L A
2101 AAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGG 2175

Q R W M E R L K T V A G S K M Q G L L E R V N T E
2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTCTGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

I H F V T K C A F Q P P P S C L R F V Q T N I S R
2251 AGATACACTTTGTACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCC 2325

L L Q E T S E Q L V A L K P W I T R Q N F S R C L
2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCC 2400

E L Q C Q P D S S T L P P P W S P R P L E A T A P
2401 TGGAGCTGCAGTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCC 2475

T A P STOP
2476 CGACAGCCCCGTGA 2489

Figure 16B

Figure 17A

→SP SP←→VH
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATTCTGTGTGTCAGTAACGCAGGTGTCCACTCCCAGGTG 0075
Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGAGTCTGGCGGTGGAGTGGTCCAGCCCGGCCGAGCCTGAGGCTGTCTGCAAGGCATCTGGCTAC 0150
T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACAGCTACGTGATGACATGGGTGCGCAAGCCCGGAAAGGGCCTCGAATGGATTGGCTACATTGTG 0225
P Y N D G T K Y N E K F K G R F T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAGTTCAAGGGCAGATTACAATATCAAGTGACAAGAGCAAGTCA 0300
T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCTCCAAATGGACAGCTTGGCTCCAGAGGACACCGCGTATATACTATTGTGTGCGCGGACCGCTTAC 0375
D W Y L D Y W G Q G T P V T V S S A S T K G P S V
0376 GACTGGTACTTGGACTACTGGGGCCAAAGGCACTCCAGTCACCGTCTCCTCTGTAGACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGTGGAAGCAGGCTCAGCGCTCTGCGCTGGACGCATCCCGGCTATGCAGGCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCGCTCTGCTCTTACCCGGAGCCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGGAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTTGCCCCCTGACCTAAGCCCCACCCAAAGGCCAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAACCTCCAATCTTCTCTCTGCAGAGCCCAATCTTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCCCTCGCCCTCCAGCTCAAGGCGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGCTGACAGTCCACCTCCATCTCTTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAACCATCTCCAAGCCAAAGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCCTCTGCGCTGAGAGTGACCGTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGACAAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K G G
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGACCTCTCCCTGTCTCCCGGTAAAGGCGGTG 2025
CH←→Linker

Linker←|→FLex
G S G G G G S G G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGCGGTTCAAGAGGCGGTGGATCTACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCT 2100
D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACC 2175
Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAGGACGAGGAGCTCTGCGGGGCGCTCTGGCGGCTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250
A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTACCAAATGTGCCTTTC 2325
P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCTCCTGCAGGAGACCTCCGAGCAGCTGG 2400
A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTGAGCCCGACTCCTCAA 2475
L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCCCGACAGCCCCGTGA 2534

Figure 17B

Figure 18A

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACACCTATCTCCTCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→Flex
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGCGCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAAATGTGCTTTAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCGCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAAGTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGCCTGGAGCTGCAGTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGCGCCCTGGAG 0525

Flex←→hinge hinge←→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGACCGTCAGTCTTCTCTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGGGTGGTCTGCGTCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCATCCCGGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTACGCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATCGCGTGGAGTGGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGCGAGCCGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC 1200

CH3←→VH
N H Y T Q K S L S L S P G K Q V Q L V Q S G G G V
1201 AACCACTACAGCAGAAGAGCCTCTCCCTGTCTCCCGTAAACAGGTGCAGCTGGTGCAGTCTGGCGGTGGAGTG 1275

V Q P G R S L R L S C K A S G Y T F T S Y V M H W
1276 GTCCAGCCCGCGCAGCCTGAGGCTGTCTGCAAGGCATCTGGCTACACCTTACCAGTACGTGATGACATGG 1350

V R Q A P G K G L E W I G Y I V P Y N D G T K Y N
1351 GTGCGCAAGCCCGGAAAGGGCCTCGAATGGATTGGCTACATTGTGCTTATAATGACGGTACTAAGTACAAT 1425

E K F K G R F T I S S D K S K S T A F L Q M D S L
1426 GAAAAGTTCAAGGGCAGATTACAATATCAAGTGACAAGGCAAGTCAACCGATTCTCCAATGGACAGCTTG 1500

R P E D T A V Y Y C A R G S R Y D W Y L D Y W G Q
1501 CGTCCAGAGGACACCGCGTATACTATTGTGTGCGCGGACCGGTTACGACTGGTACTTGGACTACTGGGGCCAA 1575

VH←→Linker Linker←→V_L
G T P V T V S S G G G G S G G G S G G G S N I
1576 GGCCTCCAGTCACCGTCTCCTCTGGCGGTGGAGGCTCTGGTGGAGGCGGTTCAAGGAGGCGGTGGATCTAACATC 1650

M M T Q S P S S L S A S V G D R V T I T C K S S Q
1651 ATGATGACTCAGAGCCCATCCAGCTTGAGCGCATCAGTAGGCGACCGGTAACGATCACTTGCAAATCCTCTCAG 1725

S V L Y S S N Q K N Y L A W Y Q Q T P G K A P K L
1726 TCAGTATTGTACTCCAGCAACCAGAAGAACTACCTGGCCGATATCAGCAGACTCCCGGCAAAGCCCCAAAGTTG 1800

L I Y W A S T R E S G V P S R F S G S G S G T D Y
1801 CTGATTTATTGGGCCTCCACGCGCAGTCTGGCGTGCCATCACGCTTTAGCGGCAGCGGGTCCGGTACAGATTAC 1875
T F T I S S L Q P E D I A T Y Y C H Q Y F S S Y T
1876 ACGTTTACCATTAGCAGTCTGCAGCCTGAGGACATAGCCACCTACTACTGTCCACCAGTACTTTAGTTCCTACACT 1950
V_L←|
F G Q G T K L Q I T R STOP
1951 TTTGGCCAGGGAACATAAAGTCAGATTACTCGATGA 1986

Figure 18B

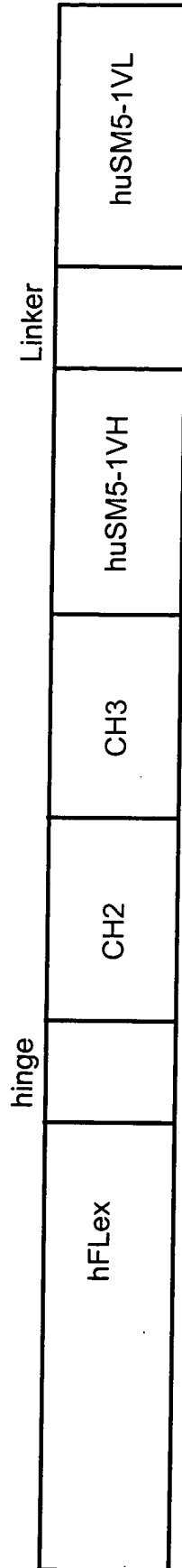


FIGURE 19

Figure 20A

SP→|→SP SP←|→VH
M E W S W I F L F L L S G T A G V H S E V
0001 CTGCGCCACCATGGAATGGAGTTGGATATTTCTCTTTCTCTCTGTCAGGAAGTCAGGTGTCCACTCTGAGGTC 0075
Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
0076 CAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATAC 0150
T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
0151 ACATTCACTAGCTATGTTATGCACTGGGTGAAGCAGAAGCCTGGGCAGGGCCTTGACTGGATTGGATATATTGTT 0225
P Y N D G T K Y N E K F K G K A T L T S D K S S S
0226 CCTTACAATGATGGCACTAAGTACAATGAGAAGTTCAAAGGCAAGGCCACTGACTTCAGACAAATCCTCCAGC 0300
T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
0301 ACAGCCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGCGGTCTATTATTGTGTCTACGGTAGTAGGTAC 0375
VH←|→CH
D W Y L D V W G A G T T V T V S S A S T K G P S V
0376 GACTGGTATTTAGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCCTCAGCTAGCACCAAGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGTGGAAGCAGGCTCAGCGCTCTGCTGGACGATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCCTCTTCAACCGGAGCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCCTAACCCAGGCCCCGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975
0976 ACCTGCGCAAGAGCCATATCCGGGAGGACCTGCCCCCTGACCTAAGCCCCACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCTCCAGATTCCAGTAAGTCCCAATCTTCTCTCTGCAGAGCCCAATCTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCCGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACAGTCCACCTCCATCTCTTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGAGCTGAGCCAGAACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCTGCGTCTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGTGGA 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K T Q D
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGTAACCAACAGG 2025

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
2026 ACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

D Y P V T V A S N L Q D E E L C G G L W R L V L A
2101 AAGATTACCCAGTCACCGTGGCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGG 2175

Q R W M E R L K T V A G S K M Q G L L E R V N T E
2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

I H F V T K C A F Q P P P S C L R F V Q T N I S R
2251 AGATACACTTGTACCAAATGTGCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCC 2325

L L Q E T S E Q L V A L K P W I T R Q N F S R C L
2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCC 2400

E L Q C Q P D S S T L P P P W S P R P L E A T A P
2401 TGGAGCTGCAGTGTGAGCCCGACTCCTCAACCTGCCACCCCATGGAGTCCCCGGGCCCTGGAGGCCACAGCCC 2475

T A P STOP
2476 CGACAGCCCCGTGA 2489

Figure 20B

Figure 21A

SP SP
M E W S W I F L F L L S G T A G V H S E V
0001 CTGTGCCGCCACCATGGAATGGAGTTGGATATTTCTCTTCTCTGTGAGGAATGCAGGTGTCCACTCTGAGGTC 0075
Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
0076 CAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATAC 0150
T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
0151 ACATTCACTAGCTATGTTATGCACTGGGTGAAGCAGAAGCTGGGCAGGGCCTTGACTGGATTGGATATATTGTT 0225
P Y N D G T K Y N E K F K G K A T L T S D K S S S
0226 CCTTACAATGATGGCACTAAGTACAATGAGAAGTTCAAAGGCAAGGCCACTGACTTCAGACAAATCCTCCAGC 0300
T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
0301 ACAGCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGCGGTCTATTATGTGTCTACGGTAGTAGGTAC 0375
VH CH
D W Y L D V W G A G T T V T V S S A S T K G P S V
0376 GACTGGTATTTAGATGTCTGGGGCGCAGGGACCAAGGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAAGACACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGTGTCTTGAACTCAGGCGCCTGACCAGCGCGTGCACACCTCCCGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGTGGAAGCAGGCTCAGCGCTCTGCTGGACGCATCCCGGCTATGCAGGCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCGCTCTGCTCTTCAACCGGAGCCTCTGCCC GCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCCTAACCCAGGCGCTGCACACAAAGGGGAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCTGACCTAAGCCCCACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTCTGTCAGAGCCCAATCTTGTA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCCAAGGTAAGCCAGCCAGGCGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCTAGAGTAGCTGCATCCAGGACAGGCCCCAGCGGGTGCTGACAGTCCACCTCCATCTCTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCTGGGGGACCGTCACTTCTCTCTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCTP 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGAGCTGAGCCAGAACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAGCCAAAGGTGGGACCCGTTGGGGTGGCAGGGCCACATGGACAGAGGCGGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCGGGATGAGCTGACCAAGAACAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G O P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACCTACAAGACCACGCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGAGCGTCTTCTCTCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
CH Linker
S V M H E A L H N H Y T Q K S L S L S P G K G G
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAAGGCGGTG 2025

Linker←|→FLEX
G S G G G G S G G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGCGGTTTCAGGAGGCGGTGGATCTACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCT 2100
D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACC 2175
Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAGGACGAGGAGCTCTGCGGGGCGCTCTGGCGGCTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250
A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGGTGAACACGGAGATACACTTTGTACCAAATGTGCCTTTC 2325
P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCTCCTGCAGGAGACCTCCGAGCAGCTGG 2400
A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTGAGCCCGACTCCTCAA 2475
L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCATGGAGTCCCGGCGCCCTGGAGGCCACAGCCCCGACAGCCCCGTGA 2534

Figure 21B

Figure 22A

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACTATCTCCTCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCTGCTGGGTCCAAGATGCAAGGCTTGTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAATGTGCTTTTCAGCCCCCCCCAGCTGTCTTCTGCTTCTGCTCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCTGGAGCTGCAGTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCCGGCCCTGGAG 0525

FLEX←→HINGE hinge←→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGAGCCCAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTCGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAGGACACCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCAATGCGTGGTGGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGAGCGCTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGTGGTCTGCGTCTCACCCTG 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAGGACTGGCTGAATGGCAAGGAGTCAAGTGAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCAAAGCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCGAGCCGAGAACTACAAGACCGCTCCCGTGTGGACTCGACGGCTCCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAC 1200

CH3←→VH
N H Y T Q K S L S L S P G K E V Q L Q Q S G P E L
1201 AACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAAGAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTG 1275

V K P G A S V K M S C K A S G Y T F T S Y V M H W
1276 GTAAAGCCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATACACATTCAGTAGCTATGTTATGCACTGG 1350

V K Q K P G Q G L D W I G Y I V P Y N D G T K Y N
1351 GTGAAGCAGAAGCCTGGGCAGGGCCTTGACTGGATTGGATATATGTTCCTTACAATGATGGCACTAAGTACAAT 1425

E K F K G K A T L T S D K S S S T A Y M E L S R L
1426 GAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCAGACCTACATGGAGCTCAGCAGACTG 1500

T S E D S A V Y Y C V Y G S R Y D W Y L D V W G A
1501 ACCTCTGAGGACTCTGCGGTCTATTATTGTGTCTACGGTAGTAGGTACGACTGGTATTAGATGTCTGGGGCGCA 1575

VH←→LINKER
G T T V T V S S G G G G S G G G G S G G G G S N I
1576 GGGACCACGGTCACCGTCTCCTCAGGCGGTGGAGGCTCTGGTGGAGGCGGTTCCAGAGGCGGTGGATCTAACATT 1650

LINKER←→VL
M M T Q S P S S L A V S A G E K V T M S C K S S Q
1651 ATGATGACACAGTCGCCATCATCTCTGGCTGTGTCTGCAGGAGAAAAGGTCACTATGAGCTGTAAGTCCAGTCAA 1725

S V L Y S S N Q K N Y L A W Y Q Q K P G Q S P K L
1726 AGTGT TTTATACAGTTCAAATCAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG 1800

L I Y W A S T R E S G V P D R F T G S G S G T D F
1801 CTGATCTACTGGGCATCCACTAGGGAATCTGGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTT 1875

T L T I S S V Q A E D L A V Y Y C H Q Y F S S Y T
1876 ACTCTTACCATCAGCAGTGTACAAGCTGAAGACCTGGCAGTTTATTACTGTCATCAATATTTCTCCTCATACAG 1950

V_L ←|

F G G G T K L E I K R stop
1951 TTCGGAGGGGGACCAAGCTGGAAATAAAGCGGTGA 1986

Figure 22B

Figure 23

\rightarrow SP
M G F S R I F L F L L S V T T G V H S Q V Q L
0001 GCCACCATGGGATTGAGCAGGATCTTTCTCTCCTCCTGTGAGTAACTACAGGTGTCCATCCCAGGTACAACTA 0075
Q Q P G A E L V K P G A S V K M S C K A S G Y T F
0076 CAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCTCTGCAAGGCTTCTGGCTACACATTT 0150
T S Y N M H W V K Q T P G R G L E W I G A I Y P G
0151 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCAGGA 0225
N G D T S Y N Q K F K G K A T L T A D K S S S T A
0226 AATGGTGATACTTCTCAATCAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCAGAGCC 0300
Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
0301 TACATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACGGCGGT 0375
D W Y F N V W G A G T T V T V S A
0376 GACTGGTACTTCAATGTCTGGGGCGCAGGGACCAGGTCACCGTCTCTGCA 0426
 $V_H \leftarrow$

Figure 24

[illegible]

Figure 25

→SP SP←→V_H
M G F S R I F L F L L S V T T G V H S Q V Q L
0001 GCCACCATGGGATTTCAGCAGGATCTTCTCTCTCTCTGTCAAGTACAGGTGTCCACTCCAGGTACAACCTA 0075

Q Q P G A E L V K P G A S V K M S C K A S G Y T F
0076 CAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATTT 0150

T S Y N M H W V K Q T P G R G L E W I G A I Y P G
0151 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCAGGA 0225

N G D T S Y N Q K F K G K A T L T A D K S S S T A
0226 AATGGTGATACTTCTACAATCAGAAGTTCAAGGGCAAGGCCACTGACTGCAGACAAATCCTCCAGCAGAGCC 0300

Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
0301 TACATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACGGCGGT 0375

D W Y F N V W G A G T T V T V S A A S T K G P S V
0376 GACTGGTACTTCAATGTCTGGGGCGCAGGGACACGGTCACCGTCTCTGCAGCTAGCACCAAGGGCCCATCGGTC 0450

F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525

P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGAACTCAGGCGCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600

S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675

N V N H K P S N T K V D K K V
0676 AACGTGAATCAAGCCAGCAACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750

0751 TCTGTGGAAGCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825

0826 GGCCCCGTCTGCCTCTTCAACCGGAGCCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900

0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975

0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCTGACCTAAGCCCCAACCCAAAGGCCAAACTCTCCACTCCC 1050

E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCTCCAGATTCAGTAATCCCAATCTTCTCTCTGCAGAGCCCAATCTTGTA 1125

K T H T C P P C P
1126 CAAAACCTACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200

A P
1201 CCCTAGAGTAGCCTGCATCCAGGGACAGGCCCGCGGTGCTGACAGTCCACCTCCATCTCTTCTCAGCAC 1275

E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 1350

E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTCAATGCGTGGTGGTGGACGTGAGCCAGAACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425

E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGCAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCTCA 1500

V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAAGTGGTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCA 1575

E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGCCGGCTCGGC 1650

G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725

L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCGGGATGAGCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800

D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCGCGTGGAGTGGGAGAGCAATGGGAGCGGAGAACCACTACAAGACACGCTCCCGTGTCTGAGT 1875

D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGTCTCTTCTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950

S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGGTAAATGA 2021

Figure 26

SP←|→VL
M D F Q V Q I F S F L L I S A S V I M S R G Q I
0001 ACCATGGATTTCAGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAATT 0075
V L S Q S P A I L S A S P G E K V T M T C R A S S
0076 GTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGTCAATGACTTGCAGGCCAGCTCA 0150
S V S Y I H W F Q Q K P G S S P K P W I Y A T S N
0151 AGTGAAGTTACATCCACTGGTTCAGCAGAAGCCAGGATCCTCCCCAAACCCTGGATTTATGCCACATCCAAC 0225
L A S G V P V R F S G S G S G T S Y S L T I S R V
0226 CTGGCTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGTAGAGTG 0300
E A E D A A T Y Y C Q Q W T S N P P T F G G G T K
0301 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTGGTGGTGGGACCAAG 0375
VL←|→CL
L E I K R T V A A P S V F I F P P S D E Q L K S G
0376 CTGGAGATCAAACGAACGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGA 0450
T A S V V C L L N N F Y P R E A K V Q W K V D N A
0451 ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCC 0525
L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0526 CTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0600
L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0601 CTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCTGAGCTCG 0675
P V T K S F N R G E C Stop
0676 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 0711

Figure 27A

→SP SP←→V_H
M G F S R I F L F L L S V T T G V H S Q V Q L
0001 GCCACCATGGGATTTCAGCAGGATCTTCTCTTCTCTCTGTCACTAAGTGTCCACTCCAGGTACAACATA 0075

Q Q P G A E L V K P G A S V K M S C K A S G Y T F
0076 CAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATTT 0150

T S Y N M H W V K Q T P G R G L E W I G A I Y P G
0151 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCAGGA 0225

N G D T S Y N Q K F K G K A T L T A D K S S S T A
0226 AATGGTGATACITCTTACAATCAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCTCCAGCAGAGCC 0300

Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
0301 TACATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGAAGATCGACTTACTACGCGGT 0375

D W Y F N V W G A G T T V T V S A A S T K G P S V
0376 GACTGGTACTTCAATGTCTGGGGCGCAGGACACGGTCACCGTCTCTGCAGCTAGCACCAAGGGCCCATCGGTC 0450

F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525

P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGTGTCTTGGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600

S S G L Y S L S S V V T V P S S S L G T O T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675

N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCCAGCAACACCAAGGTGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750

0751 TCTGCTGGAAGCAGGCTCAGCGCTCTGCTGCGATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825

0826 GGCCCCGTCTGCTCTTCAACCGGAGCCTCTGCCCCGCCCACTCATGCTCAGGAGAGGGTCTTCTGGCTTTTTC 0900

0901 CCAGGCTCTGGGCAGGCAAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGGAGGTGCTGGGCTCAG 0975

0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCTGACCTAAGCCCACCCCAAGGCCAAACTCTCCACTCCC 1050

E P K S C D
1051 TCAGTCTGGACACCTTCTCTCTCCAGATTCCAGTAATCCCAATCTTCTCTGCGAGCCCAAACTCTTGTA 1125

K T H T C P P C P
1126 CAAAATCACAATGCCACCGTGCCAGGTAAGCCAGCCAGGCGCTCGCCCTCCAGCTCAAGGCGGACAGGTG 1200

A P
1201 CCTAGATAGCTGCATCTCAGGGACAGGCCCCAGCGGGTGCTGACAGCTCCACCTCCATCTCTTCTCTCAGCAG 1275

E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAAGTCTGGGGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGAGCC 1350

E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425

E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGTTGGTCTGCGTCTCA 1500

V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575

E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCGGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650

G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725

L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCTGGTCAAAGGCTTCTATCCCA 1800

D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCGGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACAACTACAAGACACGCTCCCGTGTGGACT 1875

D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGACAAGAGCAGGTGGCAGCAGGGGACGCTTCTCAT 1950

CH←|→FLex

1951 S V M H E A L H N H Y T Q K S L S L S P G K T Q D
GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGGTAAAACCCAGG 2025

2026 C S F Q H S P I S S D F A V K I R E L S D Y L L Q
ACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

2101 D Y P V T V A S N L Q D E E L C G G L W R L V L A
AAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGCTCTGGCGGCTGGTCTCTGG 2175

2176 Q R W M E R L K T V A G S K M Q G L L E R V N T E
CACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

2251 I H F V T K C A F Q P P P S C L R F V Q T N I S R
AGATACACTTTGTACCAAATGTGCCTTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCC 2325

2326 L L Q E T S E Q L V A L K P W I T R Q N F S R C L
GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCC 2400

2401 E L Q C Q P D S S T L P P P W S P R P L E A T A P
TGGAGCTGCAGTGTGAGCCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCC 2475

2476 T A P STOP
CGACAGCCCCGTGA 2489

Figure 27B

|→SP
 M G F S R I F L F L L S V T T G V H S Q V Q L
 0001 GCCACCATGGGATTGAGCAGGATCTTTCTCTCTCTCTGTGAGTAACTACAGGTGCCACTCCAGGTTACAACTA 0075
 Q Q P G A E L V K P G A S V K M S C K A S G Y T F
 0076 CAGCAGCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATTT 0150
 T S Y N M H W V K Q T P G R G L E W I G A I Y P G
 0151 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGTGGGGCCTGGAATGGATTGGAGCTATTATCCAGGA 0225
 N G D T S Y N Q K F K G K A T L T A D K S S S T A
 0226 AATGGTGATACTTCTCTACAATCAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCTCCAGCAGACCC 0300
 Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
 0301 TACATGCGACTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACGGCGGT 0375
 D W Y F N V W G A G T T V T V S A A S T K G P S V
 0376 GACTGGTACTTCAATGTCTGGGGCGCAGGGACCAGGTACCGTCTCTGCAAGCTAGCACCAAGGGCCCATCGGT 0450
 F P L A P S S K S T S G G T A A L G C L V K D Y F
 0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
 P E P V T V S W N S G A L T S G V H T F P A V L Q
 0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCTGACCAGCGGCTGCACACCTTCCGGCTGTCTCTACAG 0600
 S S G L Y S L S S V V T V P S S S L G T Q T Y I C
 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
 N V N H K P S N T K V D K K V
 0676 AACGTGAATCACAGCCAGCAACACCAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
 0751 TCTGCTGGAAGCAGGCTCAGCGCTCTGCTCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
 0826 GGCCCCGTCTGCTCTTCTTCAACCCGGAGCCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
 0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975
 0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTTGCCCTGACCTAAGCCACCCCAAAGGCCAAATCTCCACTCCC 1050
 E P K S C D
 1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAAGTCCCAATCTTCTCTCTGAGAGCCCAATCTTGTA 1125
 K T H T C P P C P
 1126 CAAAACCTCACATATGCCACCGTGCCAGGTAAGCCAGGCCAGGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
 A P
 1201 CCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCTCTCAGCAC 1275
 E L L G G P S V F L F P P K P K D T L M I S R T P
 1276 CTGAATCTCTGGGGGACCGTCACTTCTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
 E V T C V V V D V S H E P E V K F N W Y V D D G V
 1351 CTGAGTCAATACGCTGGTGGTGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
 E V H N A K T K P R E E G Q Y N S C T Y R V V S V L T
 1426 TGGAGGTGCATAATGCAAGACAAAGCCGCGGAGGACGAGTACAAAGCAGCTACCGGTGGTCTGCGCTCTCA 1500
 V L H Q D W L N G K E Y K C K V S N K A L P A P I
 1501 CGTCTGACACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCA 1575
 E K T I S K A K
 1576 TCGAGAAAACCATCTCCAAGGCCAAAGGTGGGACCCGTGGGGTGGCAGGGGCCATGGACAGAGGCCGGCTCGGC 1650
 G Q P R E P Q V Y T
 1651 CCACCTCTGCCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
 L P P S R D E L T K N Q V S L T C L V K G F Y P S
 1726 CCCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
 D I A V E W E S N G Q P E N N Y K T T P P V L D S
 1801 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACAACTACAAGACACGCTCCCGTGTGGACT 1875
 D G S F F L Y S K L T V D K S R W Q Q G N V F S C
 1876 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
 CH←|→Linker
 1951 GCTCCGTGATGCAATGAGGCTCTGCACAACTACTACGACAGAGGCTCTCCCTGTCTCCCGGTAAAGGCGGTG 2025

Linker←|→FLEX

G S G G G G S G G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGCGGTTTCAGGAGGCGGTGGATCTACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCT 2100

D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACC 2175

Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAGGACGAGGAGCTCTGCGGGGCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250

A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTACCAAATGTGCCTTTC 2325

P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCTGCAGGAGACCTCCGAGCAGCTGG 2400

A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTGAGCCCGACTCCTCAA 2475

L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCCGACAGCCCGTGA 2534

Figure 28B

Figure 29A

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→Flex
G T Q D C S F Q H S P I S S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACGCGCTGGATGGAGCGCTCAAGACTGTGCTGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTCAACAAATGTGCCCTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCGCGCTCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGCCTGGAGTGCAGTGTGAGCCGACTCCTCAACCTGCCACCCCCATGGAGTCCCCGGCCCTGGAG 0525

Flex←→hinge hinge←→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGAGCCCAATCTTGTGACAAAACCTCACATGCCCCACCGTGGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGCGCTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGCTGGTCTGCGTCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAACCAAGGTGTACACCTGCCCCATCCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTACGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCGAGCCGAGAACAACTACAAGACACGCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←→VH
N H Y T Q K S L S L S P G K Q V Q L Q Q P G A E L
1201 AACCACTACAGCAGAAGAGCCTCTCCTGTCTCCCGTAAACAGGTACAACCTACAGCAGCCTGGGGCTGAGCTG 1275

V K P G A S V K M S C K A S G Y T F T S Y N M H W
1276 GTGAAGCCTGGGCGCTCAGTGAAGATGTCTGTGAAGGCTTCTGGCTACACATTACAGTTACAATATGCACTGG 1350

V K Q T P G R G L E W I G A I Y P G N G D T S Y N
1351 GTAAAGCAGACACCTGGTGGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCTTACAAT 1425

Q K F K G K A T L T A D K S S S T A Y M Q L S S L
1426 CAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCTCCAGCACAGCTACATGCAGCTCAGAGCCTG 1500

T S E D S A V Y Y C A R S T Y Y G G D W Y F N V W
1501 ACATCTGAAGACTCTGCGTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTCAATGTCTGG 1575

V_H←→Linker Linker←→
G A G T T V T V S A G G G G S G G G G S G G G G S
1576 GCGCGAGGACCAAGGTACCGTCTCTGAGGCGGTGGAGGCTCTGGTGGAGCGGTTGAGGAGCGGTGGATCT 1650

→V_L
Q I V L S Q S P A I L S A S P G E K V T M T C R A
1651 CAAATTGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACAATGACTTGCAGGGCC 1725

S S S V S Y I H W F Q Q K P G S S P K P W I Y A T
1726 AGCTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTCCCCAAACCCTGGATTATGCCACA 1800

S N L A S G V P V R F S G S G S G T S Y S L T I S
1801 TCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGT 1875

R V E A E D A A T Y Y C Q Q W T S N P P T F G G G
1876 AGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCCGGTGGTGGG 1950
V_L ←|

T K L E I K R STOP
1951 ACCAAGCTGGAGATCAAACGATGA 1974

Figure 29B

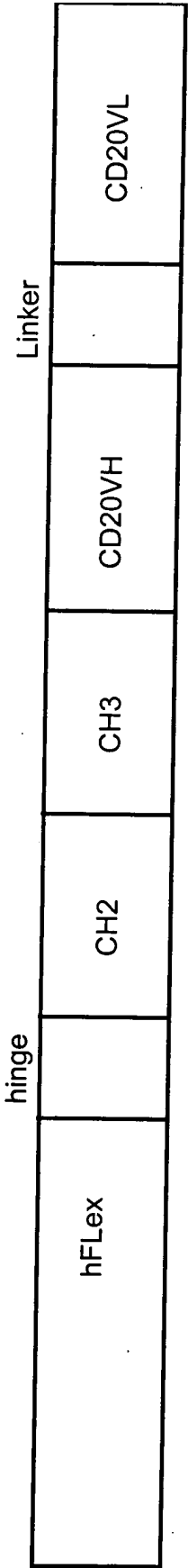


FIGURE 30

Figure 31

```

      |→SP                                     SP←|→VH
0001  M D F T Q V G Q I A F T S F L L I S A S S V I I S R G E V Q
      ATGGATTTCAGGTGACGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGAGGTTTCAG 0075

      L V E S G G G L V Q P G G S L R L S C A A S G F N
0076  CTGGTGGAGTCTGGCGGTGGCTGCTGACGCCAGGGGGCTCACTCCGTTTGTCCTGTGCACTTCTGGCTTCAAC 0150

      I K D T Y I H W V R Q A P G K G L E W V A R I Y P
0151  ATTTAAAGACACCTATATACACTGGTGCGTCAAGGCCCGGGTAAGGGCCTGGAATGGGTTGCAAGGATTTATCCT 0225

      T N G Y T R Y A D S V K G R F T I S A D T S K N T
0226  ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGGCCGTTTCACTATAAGCGCAGACACATCCAAAAACACA 0300

      A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
0301  GCCTACCTGCAGATGAACAGCCTGCGTGCTGAGGACACTGCCGTCTATTATTGTTCTAGATGGGGAGGGGACGGC 0375

      F Y A M D Y W G Q G T L V T V S S
0376  TTCTATGCTATGGACTACTGGGGTCAAGGAACCCCTGGTCACCGTCTCCTCG
      VH←|

```

Figure 32

\rightarrow SP $SP \leftarrow \rightarrow V_L$
0001 M D F Q V Q I F S F L L I S A S V I I S R G D I Q
0076 M T Q S P S S L S A S V G D R V T I T C R A S Q D
0151 V N T A V A W Y Q Q K P G K A P K L L I Y S A S F
0226 L Y S G V P S R F S G S R S G T D F T L T I S S L
0301 Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K
0376 V E I K R
0390 GTGGAGATCAAACGT

Figure 33

→SP SP←→VH
M D F Q V Q I F S F L L I S A S V I I S R G E V Q
0001 ATGGATTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGGTTTCAG 0075
L V E S G G G L V Q P G G S L R L S C A A S G F N
0076 CTGGTGGAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAAC 0150
I K D T Y I H W V R Q A P G K G L E W V A R I Y P
0151 ATTAAAGACACCTATATACACTGGGTGCGTCAGGCCCGGGTAAGGGCCTGGAATGGGTGCAAGGATTTATCCT 0225
T N G Y T R Y A D S V K G R F T I S A D T S K N T
0226 ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGGCCGTTTCACTATAAGCGCAGACACATCCAAAAACACA 0300
A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
0301 GCCTACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCCGTCTATTATTGTTCTAGATGGGAGGGGACGGC 0375
VH←→CH
F Y A M D Y W G Q G T L V T V S S A S T K G P S V
0376 TTCTATGCTATGGACTACTGGGGTCAAGGAACCTGGTCACCGTCTCTCGGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCAAGAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
TCTGCTGGAAGCAGGCTCAGCGCTCCTGCGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
GGCCCGCTGCTGCTCTTCAACCGGAGCCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCGCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975
ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCTGACCTAAGCCACCCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCCTCCAGATTCCAGTAACCTCCCAATCTTCTCTCTGCAGAGCCCAAATCTTGTA 1125
K T H T C P P C P
1126 CAAAACCTCACATGCCCCACCGTGCCAGGTAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACACGTCCACCTCCATCTCTTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCAGAACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACAGGACTGGTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCGGTGGGCTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGTAATGA 2021

Figure 34

↳SP SP←↳VL

M D F Q V Q I F S F L L I S A S V I I S R G D I Q
0001 ATGGATTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGACATCCAG 0075

M T Q S P S S L S A S V G D R V T I T C R A S Q D
0076 ATGACCCAGTCCCCGAGCTCCCTGTCCGCCTCTGTGGGCGATAGGGTTACCATCACCTGCCGTGCCAGTCAGGAT 0150

V N T A V A W Y Q Q K P G K A P K L L I Y S A S F
0151 GTGAATACTGCTGTAGCCTGGTATCAACAGAAACAGGAAAAGCTCCGAACTACTGATTTACTCGGCATCCTTC 0225

L Y S G V P S R F S G S R S G T D F T L T I S S L
0226 CTCTACTCTGGAGTCCCTTCTCGCTTCTCTGGCTCCAGATCTGGGACGGATTTCCTCTGACCATCAGCAGTCTG 0300

Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K
0301 CAGCCGGAAGACTTCGCAACTTATTACTGTGCAACATTATATACTACTCTCCACGTTCCGACAGGGTACCAAG 0375

VL←↳CL

V E I K R T V A A P S V F I F P P S D E Q L K S G
0376 GTGGAGATCAAACGTACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 0450

T A S V V C L L N N F Y P R E A K V Q W K V D N A
0451 ACTGCCTCTGTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCC 0525

L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0526 CTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0600

L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0601 CTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG 0675

P V T K S F N R G E C Stop
0676 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAG 0711

Figure 35A

|→SP SP←|→VH
 M D F Q V Q I F S F L L I S A S V I I S R G E V Q
 0001 ATGGATTTCAGGTGCAGATTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGAGGTTTCAG 0075
 L V E S G G G L V Q P G G S L R L S C A A S G F N
 0076 CTGGTGGAGTCTGGCGGTGGCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAAC 0150
 I K D T Y I H W V R Q A P G K G L E W V A R I Y P
 0151 ATTAAAGACACCTATATACACTGGGTGCGTCAGGCCCGGGTAAGGGCCTGGAATGGGTGCAAGGATTTATCCT 0225
 T N G Y T R Y A D S V K G R F T I S A D T S K N T
 0226 ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGGCCGTTTCACTATAAGCGCAGACACATCCAAAAACACA 0300
 A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
 0301 GCCTACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCCGTCTATTATGTTCTAGATGGGGAGGGGACGGC 0375
 F Y A M D Y W G Q G T L V T V S S A S T K G P S V
 0376 TTCTATGCTATGGACTACTGGGTCAAGGAACCTGGTCACCGTCTCCTCGGCTAGCACCAAGGGCCCATCGGTC 0450
 F P L A P S S K S T S G G T A A L G C L V K D Y F
 0451 TTCCCTCGGCACCTCTCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
 P E P V T V S W N S G A L T S G V H T F P A V L Q
 0526 CCCGAACCGGTACCGTGTCTTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
 S S G L Y S L S S V V T V P S S S L G T Q T Y I C
 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
 N V N H K P S N T K V D K K V
 0676 AACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
 0751 TCTGTGGAAGCAGGCTCAGCGCTCCTGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
 0826 GGCCCCGTCTGCTCTTCAACCGGAGCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
 0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGCAGGTGCTGGGCTCAG 0975
 0976 ACCTGCAAGAGCCATATCCGGGAGGACCTGCCCCCTGACCTAAGCCCCCAAGGCCAAACTCTCCACTCCC 1050
 E P K S C D
 1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAAGTCCCAATCTTCTCTCTGCAGAGCCCAATCTTGTGA 1125
 K T H T C P P C P
 1126 CAAAACCTCACACATGCCACCGTGGCCAGGTAAGCCAGCCAGGCCCTCGCCCTCCAGCTCAAGGCGGACAGGTG 1200
 A P
 1201 CCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACACGTCCACCTCCATCTCTTCTCAGCAC 1275
 E L L G G P S V F L F P P K P K D T L M I S R T P
 1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
 E V T C V V V D V S H E P E V K F N W Y V D D G V
 1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
 E V H N A K T K P R E E Q Y N S T Y R V V S V L T
 1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGGTGGTCTGCGTCTCA 1500
 V L H Q D W L N G K E Y K C K V S N K A L P A P I
 1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
 E K T I S K A K
 1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCGTGGGGTGGAGGGCCACATGGACAGAGGCGGCTCGGC 1650
 G Q P R E P Q V Y T
 1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
 L P P S R D E L T K N Q V S L T C L V K G F Y P S
 1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
 D I A V E W E S N G Q P E N N Y K T T P P V L D S
 1801 GCGACATGCGCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACAACTACAAGACACGCTCCCGTGTCTGACT 1875
 D G S F F L Y S K L T V D K S R W Q Q G N V F S C
 1876 CCGACGGCTCTTCTCTCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950

CH←|→FLEX
S V M H E A L H N H Y T Q K S L S L S P G K T Q D
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGTAAAACCCAGG 2025

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
2026 ACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

D Y P V T V A S N L Q D E E L C G G L W R L V L A
2101 AAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGCGCTCTGGCGGCTGGTCTCTGG 2175

Q R W M E R L K T V A G S K M Q G L L E R V N T E
2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

I H F V T K C A F Q P P P S C L R F V Q T N I S R
2251 AGATACACTTTGTACCAAATGTGCCTTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCC 2325

L L Q E T S E Q L V A L K P W I T R Q N F S R C L
2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCC 2400

E L Q C Q P D S S T L P P P W S P R P L E A T A P
2401 TGGAGCTGCAGTGTGAGCCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCC 2475

T A P STOP
2476 CGACAGCCCCGTGA 2489

Figure 35B

Figure 36A

SP<|>VH
M D F Q V Q I F S F L L I S A S V I I S R G E V Q
0001 ATGGATTTCAGTGCAGATTTCAGCTTCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGGTTTCAG 0075
L V E S G G G L V Q P G G S L R L S C A A S G F N
0076 CTGGTGGAGTCTGGCGGTGGCTGGTGCAGCCAGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAAC 0150
I K D T Y I H W V R Q A P G K G L E W V A R I Y P
0151 ATTAAAGACACCTATATACACTGGGTGCGTCAGGCCCGGGTAAGGGCCTGGAATGGGTGCAAGGATTTATCCT 0225
T N G Y T R Y A D S V K G R F T I S A D T S K N T
0226 ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGGCCGTTTCACTATAAGCGCAGACACATCCAAAAACACA 0300
A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
0301 GCCTACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCCGTCTATTATGTCTTAGATGGGGAGGGGACGGC 0375
VH<|>CH
F Y A M D Y W G Q G T L V T V S S A S T K G P S V
0376 TTCTATGCTATGGACTACTGGGTCAAGGAACCTGGTCACCGTCTCTCGGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
TCTGTGGAAGCAGGCTCAGCGCTCCTGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
GGCCCCGTCTGCTCTTACCCCGAGCCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTCTGGGCTCAG 0975
ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCTGACCTAAGCCCCAACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCCTCCAGATTCCAGTAACCTCCCAATCTTCTCTCTGCAGAGCCCAATCTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCCAAGTAAGCCAGCCAGGCCCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTGACAGCTCCACCTCCATCTCTTCCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTCAATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCACTGGTACGTGGAGCGG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGCAAAGCCGGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCAAAGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCCGGATGAGCTGACCAAGAAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
CH<|>Linker
S V M H E A L H N H Y T Q K S L S L S P G K G G
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAAGGCGGTG 2025

Linker←|→FLEX

2026 G A G G C T C T G G T G G A G G C G G T T C A G G A G G C G G T G G A T C T A C C C A G G A C T G C T C C T T C C A A C A C A G C C C C A T C T C C T 2100

2101 D F A V K I R E L S D Y L L Q D Y P V T V A S N L
C C G A C T T C G C T G T C A A A A T C C G T G A G C T G T C T G A C T A C C T G C T T C A A G A T T A C C C A G T C A C C G T G G C C T C C A A C C 2175

2176 Q D E E L C G G L W R L V L A Q R W M E R L K T V
T G C A G G A C G A G G A G C T C T G C G G G G C C T C T G G C G G C T G G T C C T G G C A C A G C G C T G G A T G G A G C G G C T C A A G A C T G 2250

2251 A G S K M Q G L L E R V N T E I H F V T K C A F Q
T C G C T G G G T C C A A G A T G C A A G G C T T G C T G G A G C G C T G A A C A C G G A G A T A C A C T T T G T C A C C A A A T G T G C C T T T C 2325

2326 P P P S C L R F V Q T N I S R L L Q E T S E Q L V
A G C C C C C C C C A G C T G T C T T C G C T T C G T C C A G A C C A A C A T C T C C C G C C T C C T G C A G G A G A C C T C C G A G C A G C T G G 2400

2401 A L K P W I T R Q N F S R C L E L Q C Q P D S S T
T G G C G C T G A A G C C C T G G A T C A C T C G C C A G A A C T T C T C C C G G T G C C T G G A G C T G C A G T G T C A G C C C G A C T C T C A A 2475

2476 L P P P W S P R P L E A T A P T A P STOP
C C T G C C A C C C C A T G G A G T C C C C G G C C C T G G A G G C C A C A G C C C G A C A G C C C G T G A 2534

Figure 36B

Figure 37A

↳SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←|→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACACGCTGGATGGAGCGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAATGTGCCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGTCTGGAGTGCAGTGTGAGCCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

FLEX←|→hinge hinge←|→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCACCCTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTCCAACAAGCCCTCCAGCCCCCATCGAG 0900

CH2←|→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTGACCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGAACAGAGCAGGTGGCAGCAGGGGAAGCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←|→VH
N H Y T Q K S L S L S P G K E V Q L V E S G G G L
1201 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGTAAGAGGTTTCACTGGTGGAGTCTGGCGGTGGCCTG 1275

V Q P G G S L R L S C A A S G F N I K D T Y I H W
1276 GTGCAGCCAGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAACATTAAAGACACCTATATACACTGG 1350

V R Q A P G K G L E W V A R I Y P T N G Y T R Y A
1351 GTGCGTCAGGCCCCGGTAAGGGCCTGGAATGGGTGCAAGGATTATCCTACGAATGGTTATACTAGATATGCC 1425

D S V K G R F T I S A D T S K N T A Y L Q M N S L
1426 GATAGCGTCAAGGGCCGTTTCACTATAAGCGCAGACATCCAAAAACACAGCCTACCTGCAGATGAACAGCCTG 1500

R A E D T A V Y Y C S R W G G D G F Y A M D Y W G
1501 CGTGCTGAGGACACTGCCGTCTATTATTGTTCTAGATGGGAGGGGACGGCTTCTATGCTATGGACTACTGGGGT 1575

VH←|→Linker
Q G T L V T V S S A S T K G P S V G G G G S G G G
1576 CAAGGAACCCCTGGTCACCGTCTCCTCGGCTAGCACCAAGGGCCCATCGGTGCGCGGTGGAGGCTCTGGTGGAGGC 1650

Linker←|→VL
G S G G G G S D I Q M T Q S P S S L S A S V G D R
1651 GGTTCAGGAGGCGGTGGATCTGACATCCAGATGACCCAGTCCCCGAGCTCCCTGTCCGCCTCTGTGGCGATAGG 1725

V T I T C R A S Q D V N T A V A W Y Q Q K P G K A
1726 GTTACCATCACCTGCCGTGCCAGTCAGGATGTGAATACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCT 1800
P K L L I Y S A S F L Y S G V P S R F S G S R S G
1801 CCGAAACTACTGATTTACTCGGCATCCTTCCTCTACTCTGGAGTCCCTTCTCGCTTCTCTGGCTCCAGATCTGGG 1875
T D F T L T I S S L Q P E D F A T Y Y C Q Q H Y T
1876 ACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCGGAAGACTTCGCAACTTATTACTGTCAGCAACATTATACT 1950
T P P T F G Q G T K V E I K R Stop
1951 ACTCCTCCCACGTTCCGACAGGGTACCAAGGTGGAGATCAAACGTTGA 1998

Figure 37B

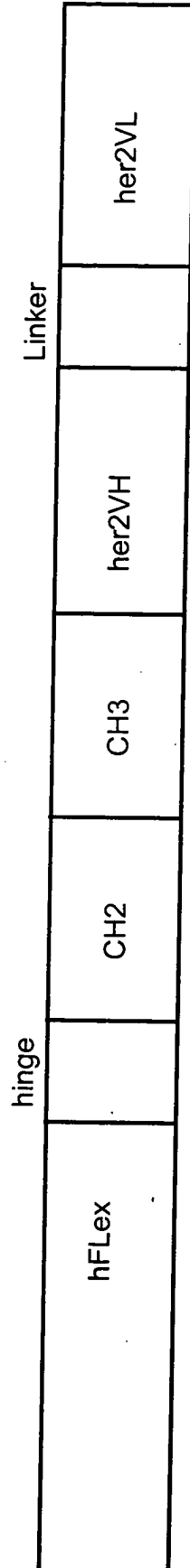


FIGURE 38

Figure 39

|→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGA CT CAGT 0075

SP←|→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTCAACAAATGTGCCTTTAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCTGGAGCTGCACTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

FLEX←|→Linker Linker←|→Trailex
A T A P T A P G G G G S G G G G S G G G G S V R E
0526 GCCACAGCCCCGACAGCCCCGGCGGTGGAGGCTCTGGTGGAGGCGGTTTCAGGAGGCGGTGGATCTGTGAGAGAA 0600

R G P Q R V A A H I T G T R G R S N T L S S P N S
0601 AGAGGTCCTCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAACTCC 0675

K N E K A L G R K I N S W E S S R S G H S F L S N
0676 AAGAAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTTCATTCTGAGCAAC 0750

L H L R N G E L V I H E K G F Y Y I Y S Q T Y F R
0751 TTGCACTTGAGGAATGGTGAAC TGGTCATGCATGAAAAAGGGTTTACTACATCTATTCCCAAACATACTTCGA 0825

F Q E E I K E N T K N D K Q M V Q Y I Y K Y T S Y
0826 TTTTCAGGAGGAAATAAAAGAAAAACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTAT 0900

P D P I L L M K S A R N S C W S K D A E Y G L Y S
0901 CCTGACCCTATATTGTTGATGAAAAGTGTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCC 0975

I Y Q G G I F E L K E N D R I F V S V T N E H L I
0976 ATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTGTCTTCTGTAACAAATGAGCACTTGATA 1050

D M D H E A S F F G A F L V G Stop
1051 GACATGGACCATGAAGCCAGTTTTTTTGGGGCCTTTTAGTTGGCTAA 1098

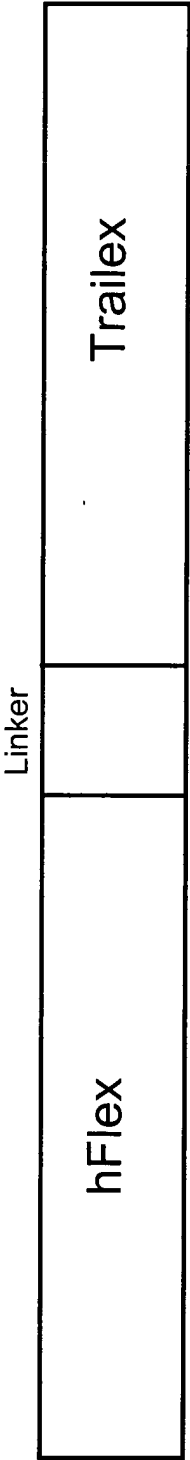


FIGURE 40

Figure 41

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGTCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTCAACAAATGTGCCTTTTCAGCCCCCCCCAGCTGTCTTCGCTTCCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGCCTGGAGTGCAGTGTGAGCCGACTCTCAACCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

FLEX←→Zipper
A T A P T A P M K Q I E D K I E E I L S K I Y H I
0526 GCCACAGCCCCGACAGCCCCGATGAAGCAGATCGAGGACAAAATTGAGGAAATCCTGTCCAAGATTACCACATC 0600

Zipper←→Trailex
E N E I A R I K K L I G E T S E E T I S T V Q E K
0601 GAGAACGAGATCGCCCGGATTAAAGAACTCATTGGCGAGACCTCTGAGGAAACCATTTCTACAGTTCAAGAAAAG 0675

Q Q N I S P L V R E R G P Q R V A A H I T G T R G
0676 CAACAAAATATTTCTCCCTAGTGAGAGAAAGAGGTCTCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGA 0750

R S N T L S S P N S K N E K A L G R K I N S W E S
0751 AGAAGCAACACATTGTCTTCTCAAACCTCAAGAATGAAAGGCTCTGGCCGCAAAATAAACTCCTGGGAATCA 0825

S R S G H S F L S N L H L R N G E L V I H E K G F
0826 TCAAGGAGTGGGCATTTCCTGAGCAACTTGCACITGAGGAATGGTGAAGTGGTCATCCATGAAAAAGGGTTT 0900

Y Y I Y S Q T Y F R F Q E E I K E N T K N D K Q M
0901 TACTACATCTATTCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATG 0975

V Q Y I Y K Y T S Y P D P I L L M K S A R N S C W
0976 GTCCAATATATTACAAATACACAAGTTATCCTGACCCTATATTGTGTGATGAAAAGTGCTAGAAAATAGTTGTTGG 1050

S K D A E Y G L Y S I Y Q G G I F E L K E N D R I
1051 TCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATT 1125

F V S V T N E H L I D M D H E A S F F G A F L V G
1126 TTTGTTTCTGTAACAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTTGGGGCCTTTTGTAGTTGGC 1200

STOP
1201 TAA

1203

Figure 42

|→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACACCTATCTCTCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←|→FLex
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAAACACAGCCCATCTCTCCGACTTCGCTGTCAAATCCGTGAGCTGCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTTGGCAGCGCTGGATGGAGCGGCTCAAGACTGCTGCTGGTCCAAGATGCAAGGCTTGTCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAAATGTGCCTTTTCCAGCCCCCCCCAGCTGTCTTCGCTTGTCTCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTGTCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCTGGAGCTGCAGTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

FLex←|→hinge hinge←|→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCAGCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCTGCGTCTCACCCTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGACCAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAG 0900

CH2←|→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCTTGCCCCATCCCGGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←|→Trailex
N H Y T Q K S L S L S P G K V R E R G P Q R V A A
1201 AACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAAGTGAGAGAAAGAGTCTCAGAGAGTAGCAGCT 1275

H I T G T R G R S N T L S S P N S K N E K A L G R
1276 CACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAACTCCAAGAATGAAAAGGCTCTGGGCCGC 1350

K I N S W E S S R S G H S F L S N L H L R N G E L
1351 AAAATAAATCTCTGGGAATCATCAAGGAGTGGGCATTCTTCTGAGCAACTTGCACCTGAGGAATGGTGAACCTG 1425

V I H E K G F Y Y I Y S Q T Y F R F Q E E I K E N
1426 GTCATCCATGAAAAGGGTTTACTACATCTATTCCCAACATACTTTGATTTTCAGGAGGAAATAAAGAAAAC 1500

T K N D K Q M V Q Y I Y K Y T S Y P D P I L L M K
1501 ACAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATCTGACCTATATTGTTGATGAAA 1575

S A R N S C W S K D A E Y G L Y S I Y Q G G I F E
1576 AGTGCTAGAAATAGTTGTGTGCTAAAGATGCAGAAATGGACTCTATTCCATCTATCAAGGGGAATATTTGAG 1650

L K E N D R I F V S V T N E H L I D M D H E A S F
1651 CTTAAGGAAATGACAGAATTTTGTCTGTAAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTT 1725

F G A F L V G STOP
1726 TTTGGGGCCTTTTGTAGTTGGCTAA 1749

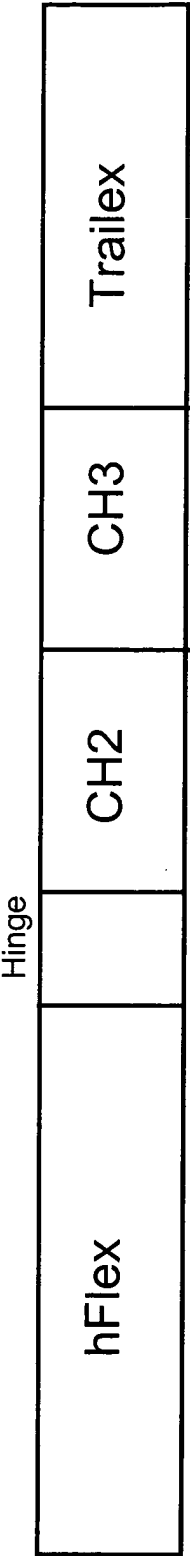


FIGURE 43

Figure 44

	HGFs+					
	-	SCF	G-CSF	GM-CSF	IL-3	CSF-1
-	1	2	33	20	12	1
FL	2	22	52	65	52	12
chSM	0	3	29	22	10	0
huSM	0	2	25	26	14	1
chSM/FL	5	23	59	75	46	12
huSM/FL	3	25	56	70	50	14

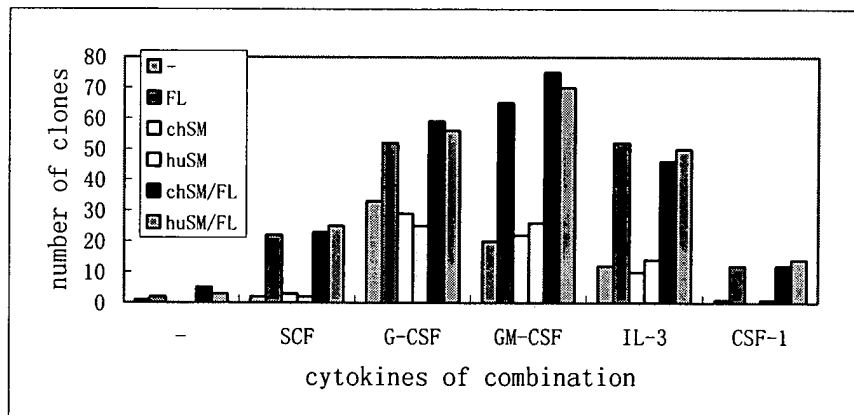
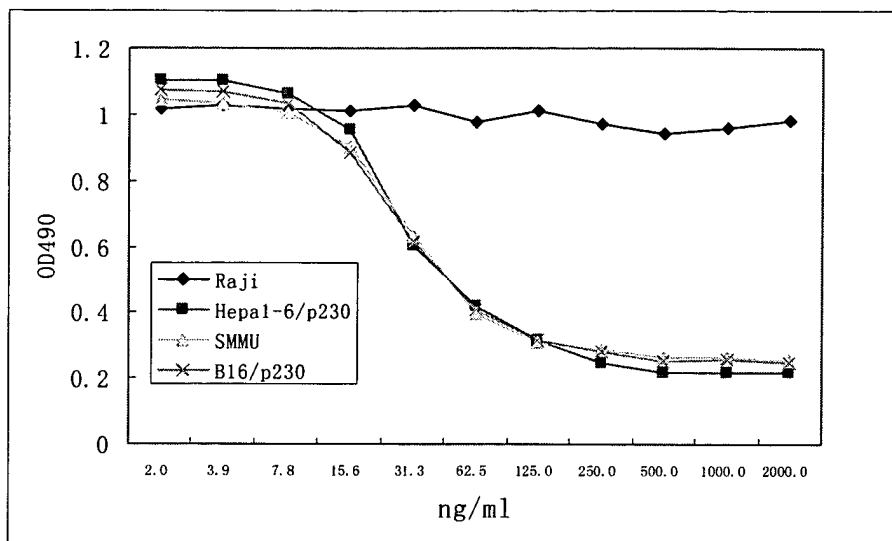
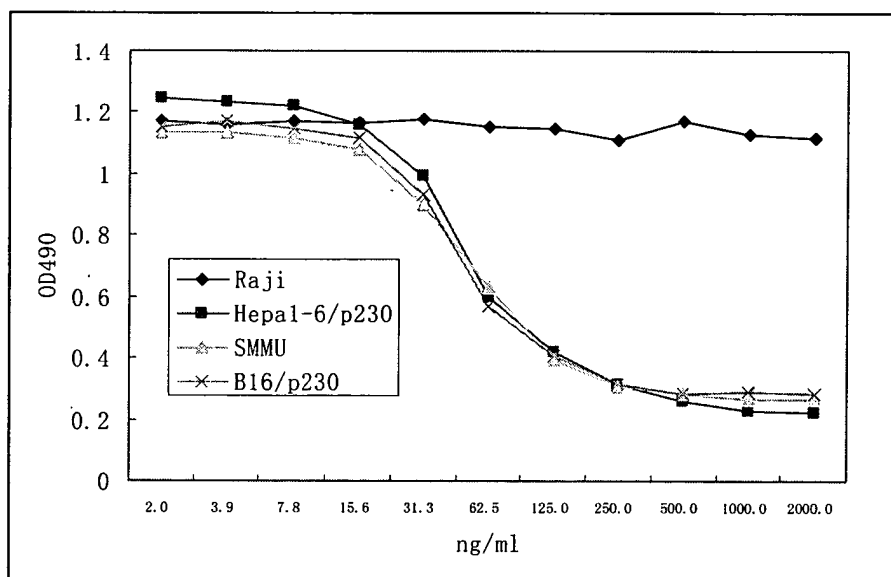


Figure 45

Item	CD3 ⁺ NK1.1 ⁺ (NK) ($\times 10^6$)			CD3 ⁺ NK1.1 ⁺ (T) ($\times 10^6$)			CD3 ⁺ NK1.1 ⁺ (NK) ($\times 10^6$)			CD11c ⁺ (DC) ($\times 10^6$)		
	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL
spleen	0	2.0	3.0	3.5	40	38	40	7.0	6.0	6.5	3.0	2.8
	3	3.0	4.0	4.0	50	55	53	5.0	9.0	10.0	5.0	8.5
	6	6.0	5.0	5.5	76	81	82	11	18.0	18.5	35	55
	8	16	15	14	68	72	70	21	28	30	85	133
	10	17	21	23	75	80	83	17	32	31	180	182
	12	24	29	30	50	53	55	50	49	47	190	165
	15	20	18	17	38	39	40	27	33	35	180	161
	18	9	12	10	22	26	28	41	49	51	150	109
liver	0	1.0	1.0	0.9	1.0	1.3	1.1	5.0	4.5	4.8	2.0	3.5
	3	2.0	3.0	3.5	1.5	1.8	2.0	6.0	6.9	7.0	3.0	4.3
	6	3.0	5.0	4.5	1.5	1.8	1.9	5.0	4.5	4.8	5.0	5.9
	8	13.0	12.0	11.0	1.5	1.9	2.1	9.0	9.9	9.5	5.5	3.7
	10	20	18.0	19.0	3.8	3.5	3.8	3.0	2.8	3.0	18.5	16.9
	12	11	17.0	16.0	5.6	5.5	5.2	19	19	20	9.0	10.1
	15	5.0	6.0	6.5	3.0	2.8	3.0	9.0	8.0	7.5	2.5	5.1
	18	2.0	3.0	3.0	3.0	3.4	3.5	2.0	2.0	2.3	8.0	7.0
Bone marrow	0	2.0	1.0	1.5	2.0	2.0	2.5	1.0	1.0	1.2	2.0	2.0
	3	1.0	2.0	2.0	5.9	5.5	5.3	1.8	1.2	1.1	3.0	1.9
	6	1.5	1.8	2.0	1.9	1.8	1.8	1.8	1.2	1.3	15.0	11.5
	8	4.0	4.5	5.0	1.5	1.5	1.8	2.5	1.9	2.1	20	33
	10	4.0	5.0	4.5	2.5	1.9	2.1	2.0	1.9	2.0	39	36
	12	4.0	5.2	5.5	2.5	1.5	1.6	5.0	5.7	6.1	29	31
	15	4.0	4.0	4.5	3.9	3.4	3.5	5.0	4.2	4.5	19	15
	18	3.0	3.3	3.5	1.9	1.8	2.0	4.0	3.7	3.4	14	13

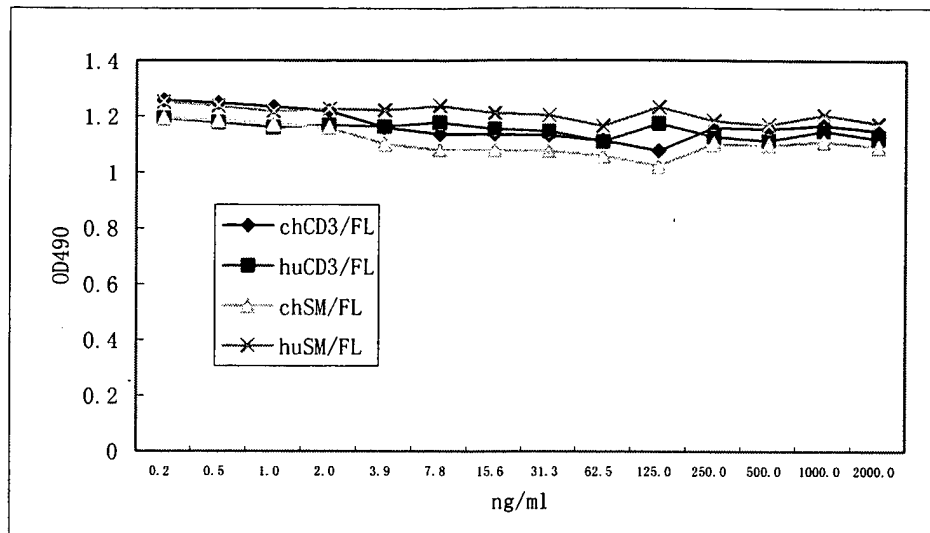
Figure 46A

chSM5-1

Figure 46B

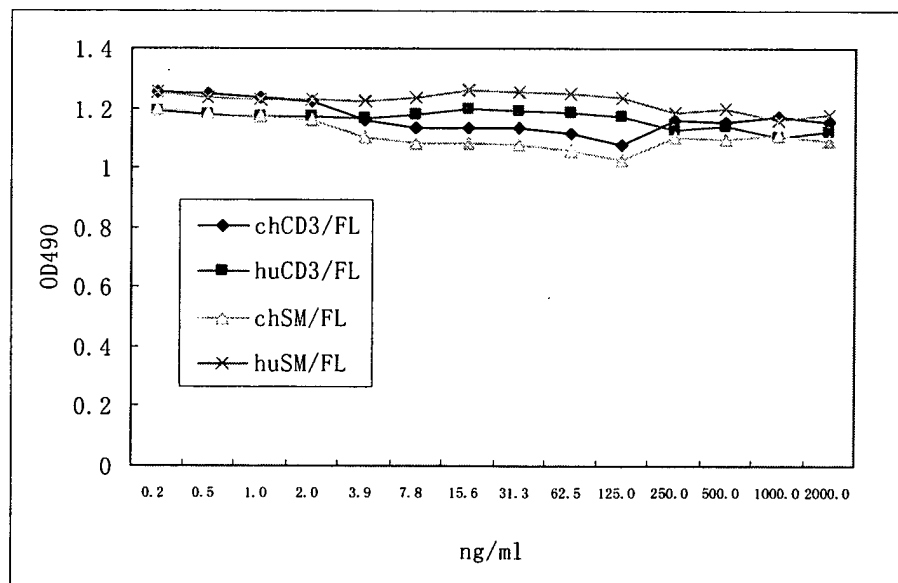
huSM5-1

Figure 47A



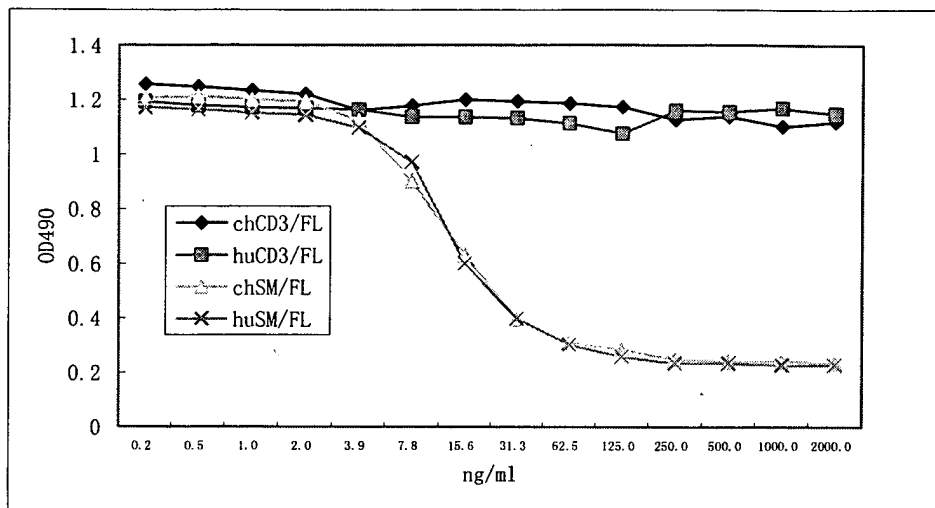
B16

Figure 47B



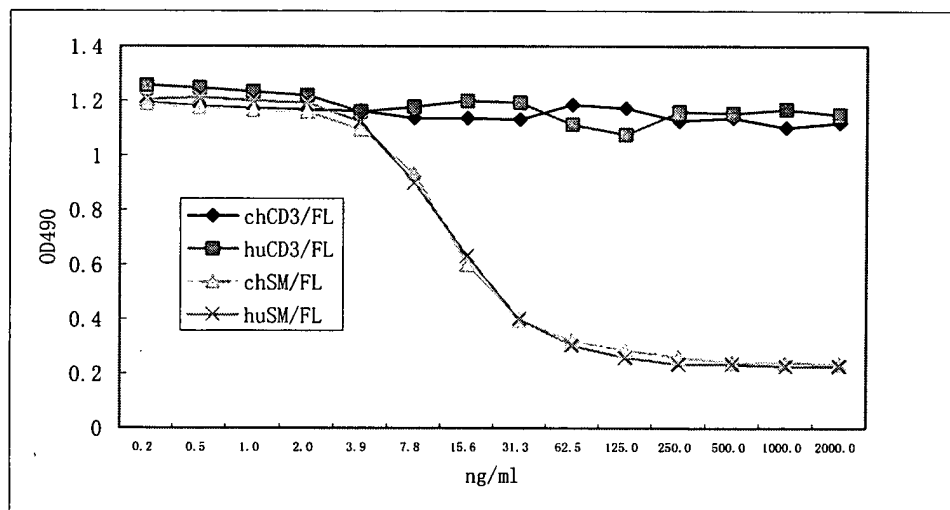
hep1-6

Figure 47C



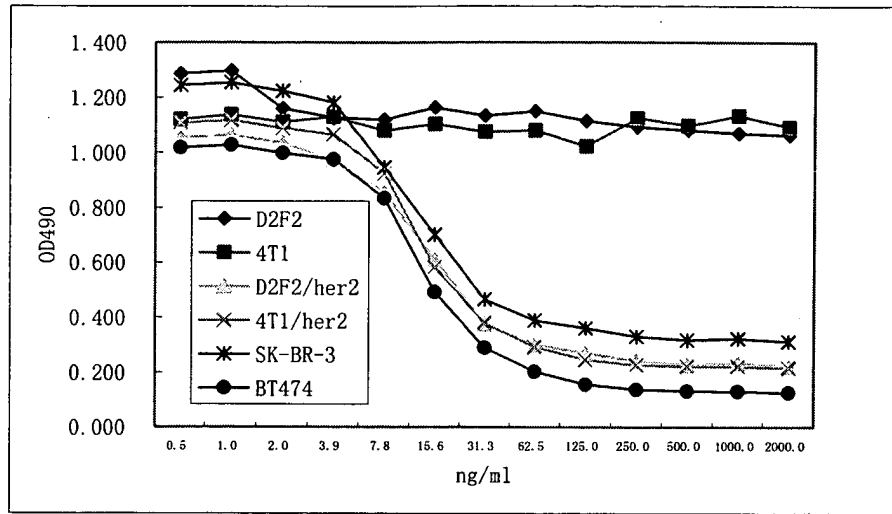
B16/p230

Figure 47D



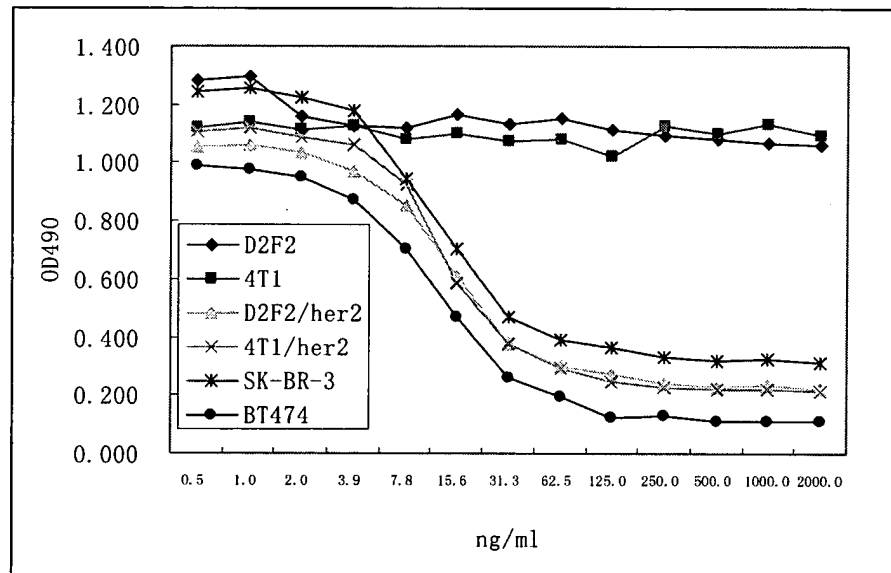
hep1-6/p230

Figure 48A

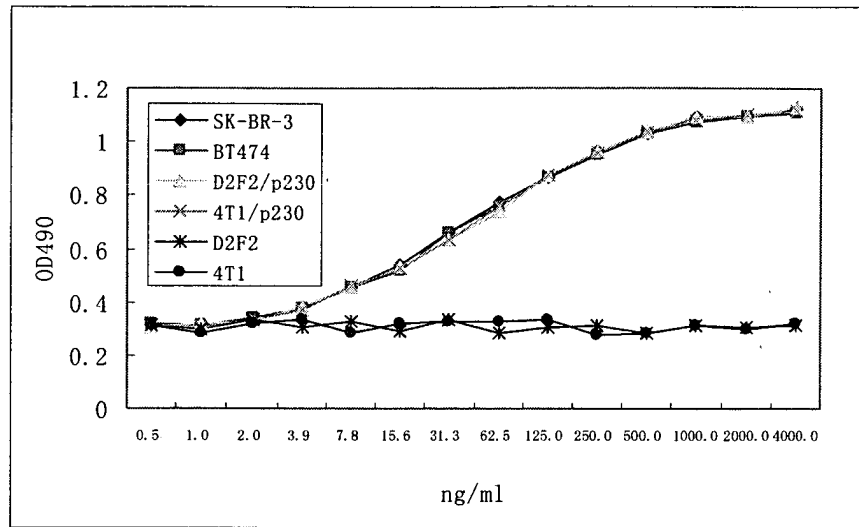


FL/her2

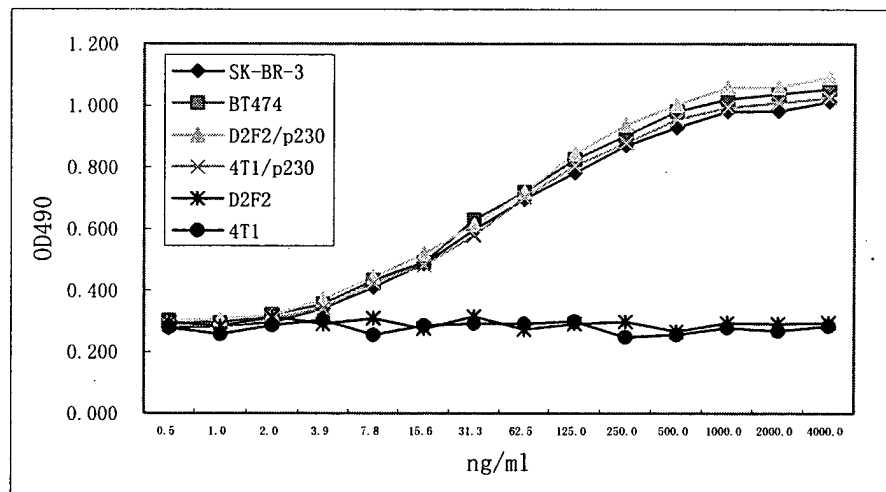
Figure 48B



herceptin

Figure 49A

her2/FL

Figure 49B

herceptin

Figure 50

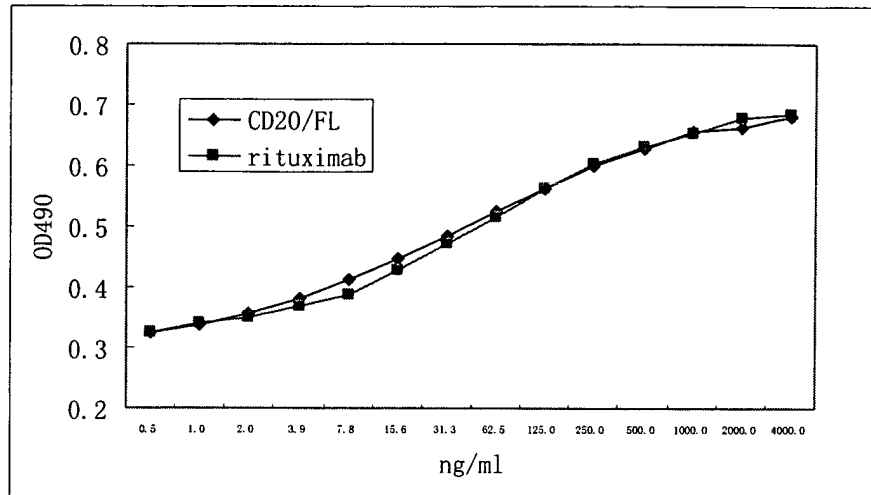
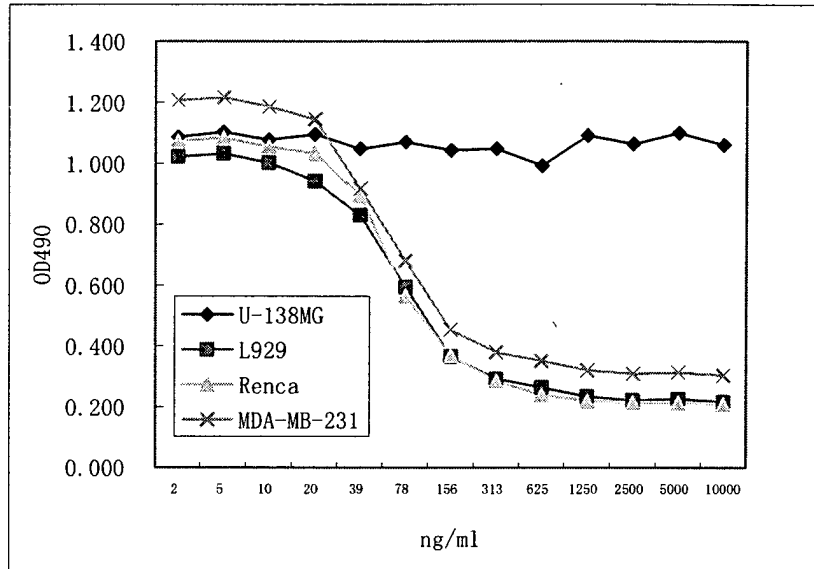
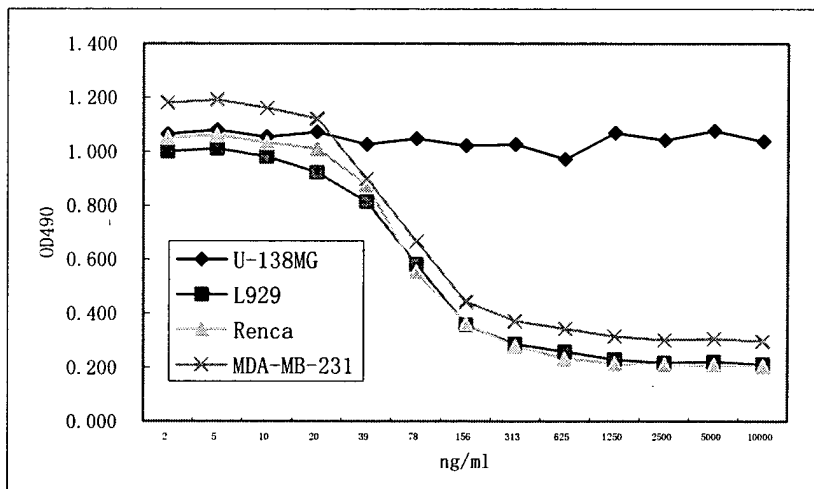


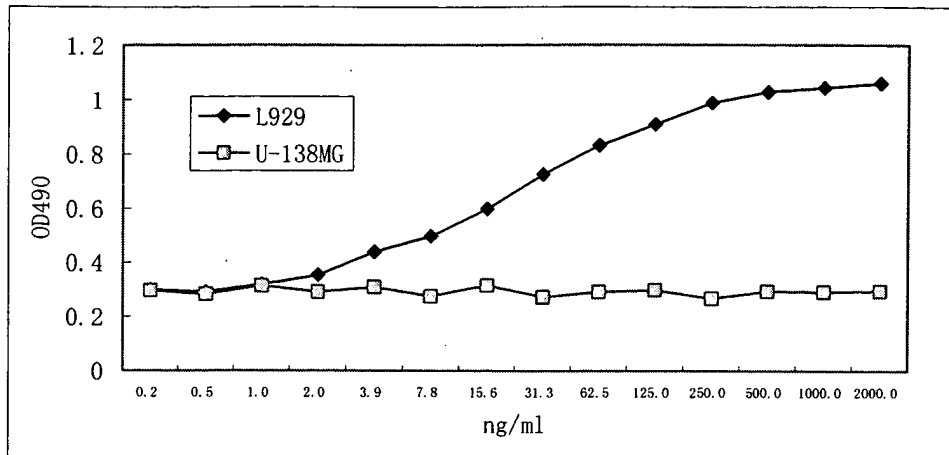
Figure 51A

Trail/FL

Figure 51B

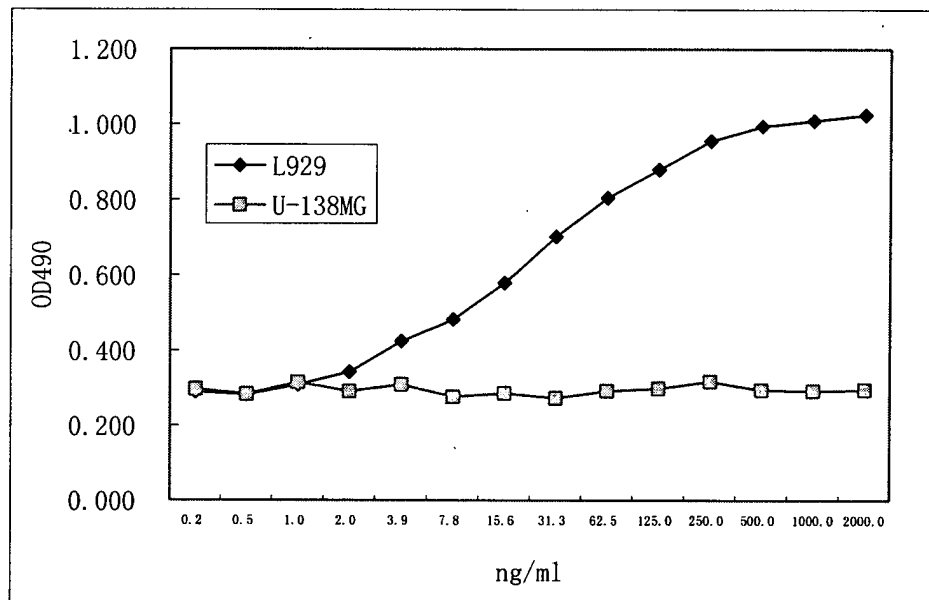
Trail

Figure 52A



Trail/FL

Figure 52B



Trail

Figure 53

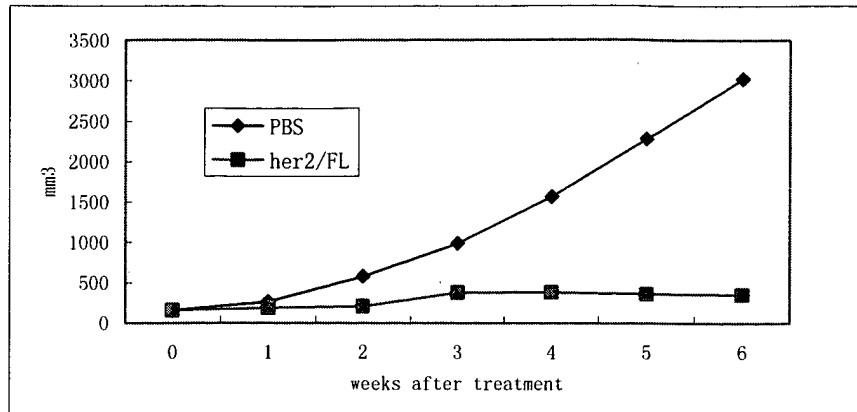


Figure 54

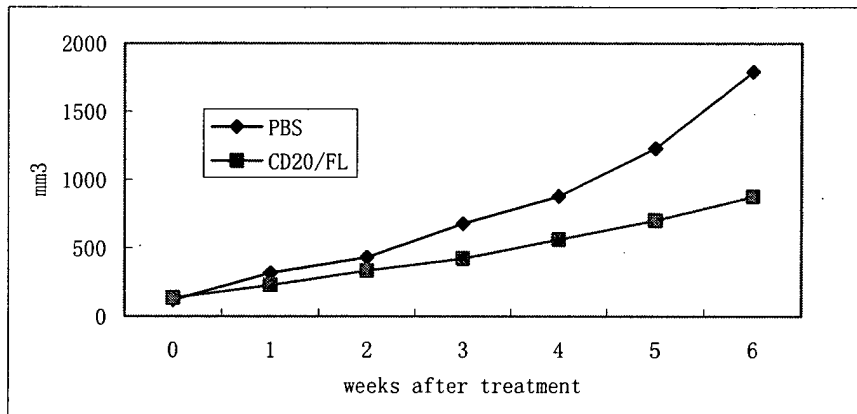
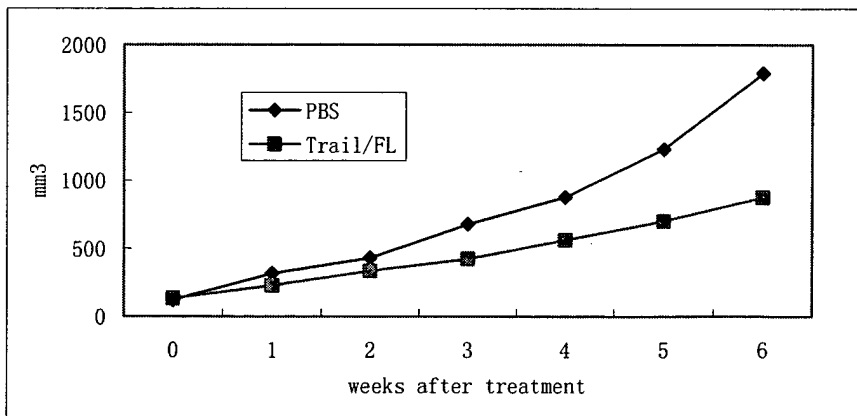


Figure 55



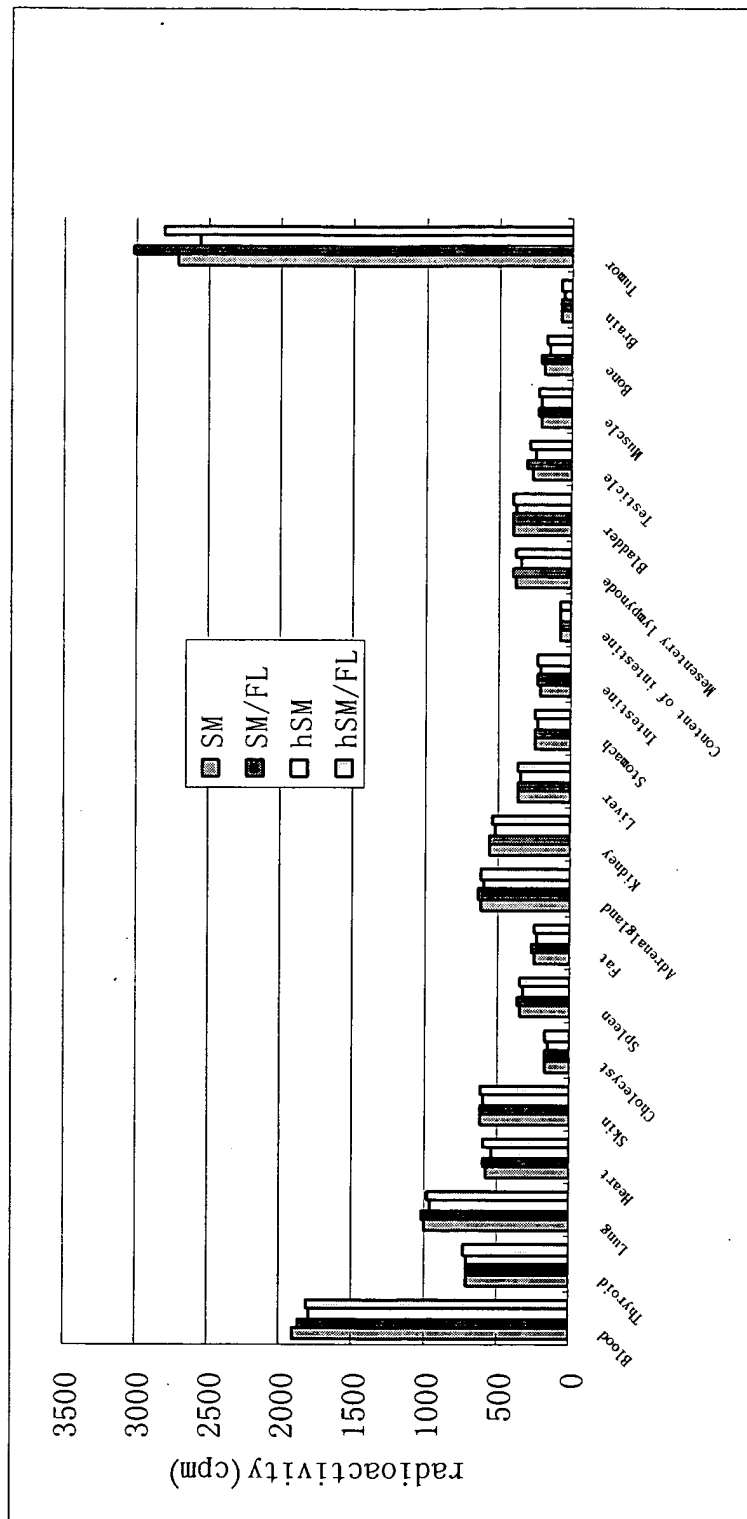


FIGURE 56

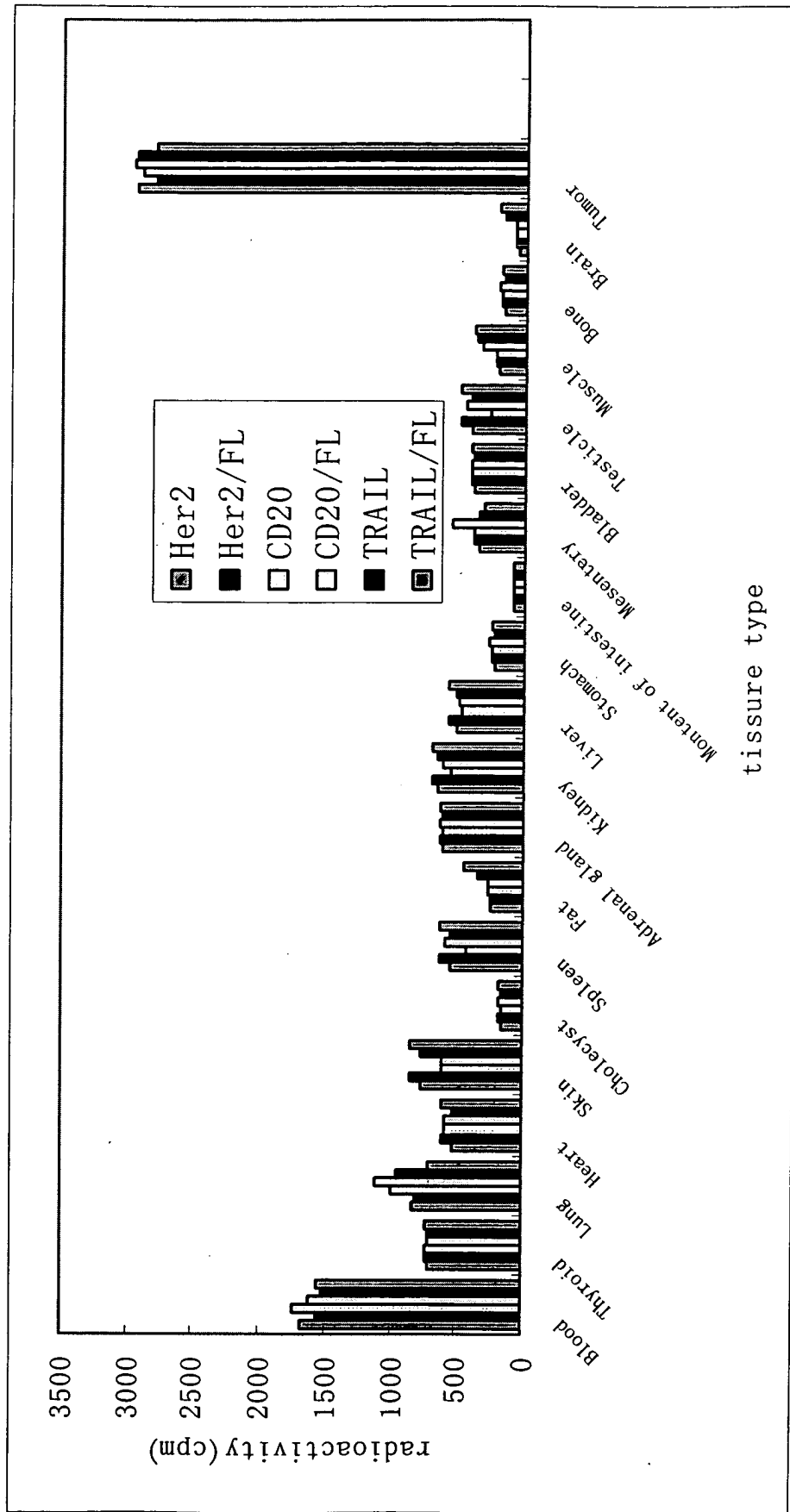


FIGURE 57